GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 13, 2004, 09:22:17 ; Search time 58.3774 Seconds
(without alignments)
2202.208 Million cell updates/sec

Title: US-10-021-121-2
Perfect score: 2450
Sequence: 1 MGPPHSGPGGVRVGALLLLG.....TTLLRQRASVEAEAGQHGPL 455

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2450	100.0	455	2	AAW33698	Aaw33698 AL-2-long
2	1841	75.1	340	2	AAW31544	Aaw31544 Human cyt
3	1841	75.1	340	2	AAW33699	Aaw33699 AL-2-shor
4	1841	75.1	340	2	AAW10637	Aaw10637 NLERK2 li
5	1841	75.1	340	6	ABU07845	Abu07845 Human eph
6	1835	74.9	340	2	AAW17081	Aaw17081 EPH famil
7	1827	74.6	340	2	AAW46615	Aaw46615 Human tra
8	1771	72.3	340	6	ABU07846	Abu07846 Mouse eph
9	628.5	25.7	334	2	AAW00287	Aaw00287 Mouse Eph

10	628.5	25.7	336	2	AAR92742	Aar92742 Murine he
11	626.5	25.6	336	6	ABU07844	Abu07844 Mouse eph
12	623	25.4	346	2	AAR55059	Aar55059 Elk tyros
13	623	25.4	346	2	AAR91930	Aar91930 Human cyt
14	623	25.4	346	2	AAW19249	Aaw19249 Human elk
15	623	25.4	346	2	AAW36055	Aaw36055 Human elk
16	623	25.4	346	2	AAW44323	Aaw44323 Human elk
17	623	25.4	346	6	ABU07841	Abu07841 Human eph
18	623	25.4	346	7	ABU62401	Abu62401 Human elk
19	622	25.4	346	2	AAR82606	Aar82606 Eph trans
20	621.5	25.4	331	2	AAW00288	Aaw00288 Chicken E
21	620.5	25.3	333	2	AAR94655	Aar94655 Ligand fo
22	620.5	25.3	333	2	AAR92743	Aar92743 Human hep
23	620.5	25.3	333	2	AAR89287	Aar89287 Human LER
24	620.5	25.3	333	2	AAW06337	Aaw06337 Full leng
25	620.5	25.3	333	2	AAW11308	Aaw11308 Receptor-
26	620.5	25.3	333	6	ABU07886	Abu07886 Novel hum
27	620.5	25.3	333	7	ADD89059	Add89059 TAT245. 1
28	610.5	24.9	308	2	AAR94656	Aar94656 Ligand fo
29	610.5	24.9	308	2	AAW06334	Aaw06334 Ligand #2
30	604.5	24.7	345	6	ABU07842	Abu07842 Mouse eph
31	483	19.7	89	3	AAY71438	Aay71438 Human eph
32	458.5	18.7	658	3	AAY96782	Aay96782 Ephrin-B2
33	456	18.6	254	6	ABU07843	Abu07843 Human eph
34	454	18.5	683	3	AAY96781	Aay96781 Ephrin-B1
35	447	18.2	229	5	AAE24019	Aae24019 Murine ep
36	443	18.1	229	5	AAE24020	Aae24020 Human eph
37	431.5	17.6	195	2	AAW06333	Aaw06333 Ligand #1
38	431.5	17.6	195	2	AAW11307	Aaw11307 Receptor-
39	284.5	11.6	92	4	AAM37671	Aam37671 Peptide #
40	284.5	11.6	92	5	ABG46524	Abg46524 Human pep
41	196.5	8.0	136	4	AAM37534	Aam37534 Peptide #
42	196.5	8.0	136	5	ABG46394	Abg46394 Human pep
43	195	8.0	82	3	AAY71437	Aay71437 Human eph
44	193.5	7.9	106	3	AAB54187	Aab54187 Human pan
45	192	7.8	82	3	AAY71436	Aay71436 Human eph

ALIGNMENTS

RESULT 1
AAW33698
ID AAW33698 standard; protein; 455 AA.
XX
AC AAW33698;
XX
DT 30-APR-1998 (first entry)
XX
DE AL-2-long (AL-2l) protein.
XX
KW AL-2l; AL-2; AL-2-long; human; treatment; neurological disorder; tumour;
KW rheumatoid arthritis; wound healing; paralysis; angiogenesis; leukaemia;
KW psoriasis; Alzheimer's disease; epilepsy.
XX
OS Homo sapiens.
XX

FH Key Location/Qualifiers
FT Peptide 1. .26
FT /note= "signal peptide"
FT Protein 27. .455
FT /note= "mature protein"
FT Domain 27. .219
FT /note= "extracellular domain"
FT Domain 220. .245
FT /note= "hydrophobic transmembrane domain"
XX
PN WO9740153-A1.
XX
PD 30-OCT-1997.
XX
PF 17-APR-1997; 97WO-US006345.
XX
PR 19-APR-1996; 96US-00635130.
XX
PA (GETH) GENENTECH INC.
XX
PI Caras IW;
XX
DR WPI; 1997-535837/49.
DR N-PSDB; AAV06354.
XX
PT Human AL-2 neurotrophic factor and related DNA - used to develop products
PT for, e.g. treating neurologic disorders, angiogenesis disorders, tumours
PT or rheumatoid arthritis or for wound healing.
XX
PS Claim 20; Fig 1A-C; 86pp; English.
XX
CC This is a AL-2-long (AL-21) protein. The AL-2 is a novel Eph-related
CC tyrosine kinase receptor ligand. AL-2 can be administered to patients in
CC whom the nervous system has been damaged by trauma, surgery, stroke,
CC ischaemia, infection, metabolic disease, nutritional deficiency,
CC malignancy, or toxic agents, to promote the survival or growth of
CC neurons. They can be used to treat motoneuron disorders such as
CC amyotrophic lateral sclerosis (Lou Gehrig's disease), Bell's palsy, and
CC various conditions involving spinal muscular atrophy, or paralysis. AL-2
CC can be used to treat human neurodegenerative disorders, such as
CC Alzheimer's disease, Parkinson's disease, epilepsy, demyelinating
CC diseases such as multiple sclerosis, Huntingtons chorea, Down's syndrome,
CC nerve deafness, Menier's disease, and other disorders of the cerebellum.
CC AL-2 can be used as cognitive enhancer, to enhance learning particularly
CC in dementias or trauma, since they can promote axonal outgrowth and
CC synaptic plasticity, particularly of hippocampal neurons that express AL-
CC 2 binding Eph-family receptors and cortical neurons that express AL-2. AL
CC -2 can also be used for wound healing, i.e. accelerating
CC neovascularisation of, e.g. burns and ulcers. The encoding nucleic acids
CC are useful in preparing antibodies that specifically bind to the AL-2
CC protein. The antibodies and the AL-2 antagonists are useful in diagnosing
CC and treating various neuronal disorders. AL-2 antagonists can be used for
CC modulating angiogenesis. They can also be used for the treatment of
CC tumours, acute myeloid leukaemia (AML), chronic myeloid leukaemia (CML),
CC myelodysplastic syndrome (MDS), diabetic retinopathy, neovascular
CC glaucoma, psoriasis and rheumatoid arthritis
XX

SQ Sequence 455 AA;

Query Match 100.0%; Score 2450; DB 2; Length 455;
Best Local Similarity 100.0%; Pred. No. 2.1e-197;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

Qy         61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy        121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180

Qy        181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

Qy        241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300

Qy        301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYTSISVLEWPILHTIQLFFMRSK 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYTSISVLEWPILHTIQLFFMRSK 360

Qy        361 CSRVTTFLFPVQVITTSTCRMTSFSFTTLNPSMQACRAQMGEFRIRWCFWGDRILGTALF 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CSRVTTFLFPVQVITTSTCRMTSFSFTTLNPSMQACRAQMGEFRIRWCFWGDRILGTALF 420

Qy        421 VLVLILLLGRLNMHQTTLLRQRASVEAEAGQHGPL 455
              |||||||||||||||||||||||||||||||||||
Db        421 VLVLILLLGRLNMHQTTLLRQRASVEAEAGQHGPL 455
```

RESULT 2
AAW31544
ID AAW31544 standard; protein; 340 AA.
XX
AC AAW31544;
XX
DT 14-APR-1998 (first entry)
XX
DE Human cytokine Lerk-8.
XX
KW Lerk-8; cytokine; human; hek; elk; receptor tyrosine kinase; ligand;
KW neurodegenerative disease; wound healing; neovascularisation; diagnosis;
KW therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1. .27

```
FT                   /label= Sig_peptide
FT   Protein         28. .340
FT                   /label= Mat_protein
FT   Domain          28. .224
FT                   /note= "extracellular domain"
FT   Modified-site   210. .212
FT                   /note= "N-glycosylated"
FT   Domain          225. .251
FT                   /note= "transmembrane domain"
FT   Domain          252. .340
FT                   /note= "cytoplasmic domain"
FT   Misc-difference 325
FT                   /note= "residue 325 is Leu in Lerk-8 variant"
XX
PN   WO9736919-A2.
XX
PD   09-OCT-1997.
XX
PF   19-MAR-1997;   97WO-US004533.
XX
PR   21-MAR-1996;   96US-00621146.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Cerretti DP;
XX
DR   WPI; 1997-503043/46.
DR   N-PSDB; AAT89519.
XX
PT   New isolated cytokine, Lerk-8 - binds to the hek and elk receptor
PT   tyrosine kinases, used to develop products for diagnosis and therapy.
XX
PS   Claim 3; Page 32-33; 37pp; English.
XX
CC   This protein sequence comprises a novel human cytokine designated Lerk-8.
CC   The amino acid sequence was deduced from a human foetal brain cDNA clone
CC   (see AAT89519). Lerk-8 binds to the cell surface receptors hek and elk,
CC   which are members of the eph/elk family of receptor tyrosine kinases.
CC   Lerk-8 polypeptides, especially soluble polypeptides comprising amino
CC   acid residues -27 to 142-197 of the full-length protein, can be expressed
CC   in transformed host cells. These polypeptides can be used to purify hek
CC   or elk proteins, and to purify or identify cells that express hek or elk
CC   on the surface. Such cells can be used in various in vitro studies or in
CC   vivo procedures, e.g. neural cells expressing elk can be administered to
CC   a mammal afflicted with a neurodegenerative disorder. The Lerk-8
CC   polypeptides can also be used to deliver diagnostic or therapeutic agents
CC   to these cells (e.g. leukaemia cells). The Lerk-8 DNA and polypeptides
CC   can also be used to: treat disorders mediated by defective or
CC   insufficient amounts of Lerk-8; to treat disorders such as injury to
CC   neural tissue or neurologic disease; to promote angiogenesis; and for
CC   wound healing or stimulating neovascularisation of grafted tissues
XX
SQ   Sequence 340 AA;

  Query Match             75.1%;  Score 1841;  DB 2;  Length 340;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-146;
  Matches  338;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

Qy         61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy        121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180

Qy        181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

Qy        241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300

Qy        301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
              ||||||||||||||||||||||||||||||||||||
Db        301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
```

```
RESULT 3
AAW33699
ID   AAW33699 standard; protein; 340 AA.
XX
AC   AAW33699;
XX
DT   30-APR-1998  (first entry)
XX
DE   AL-2-short (AL-2s) protein.
XX
KW   AL-2s; AL-2; AL-2-short; human; treatment; neurological disorder; tumour;
KW   rheumatoid arthritis; wound healing; paralysis; angiogenesis; leukaemia;
KW   psoriasis; Alzheimer's disease; epilepsy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .26
FT                   /note= "signal peptide"
FT   Protein         27. .340
FT                   /note= "mature protein"
FT   Domain          27. .219
FT                   /note= "extracellular domain"
FT   Domain          220. .245
FT                   /note= "hydrophobic transmembrane domain"
XX
PN   WO9740153-A1.
XX
PD   30-OCT-1997.
XX
PF   17-APR-1997;   97WO-US006345.
```

XX
PR 19-APR-1996; 96US-00635130.
XX
PA (GETH) GENENTECH INC.
XX
PI Caras IW;
XX
DR WPI; 1997-535837/49.
DR N-PSDB; AAV06355.
XX
PT Human AL-2 neurotrophic factor and related DNA - used to develop products
PT for, e.g. treating neurologic disorders, angiogenesis disorders, tumours
PT or rheumatoid arthritis or for wound healing.
XX
PS Claim 20; Fig 2A-B; 86pp; English.
XX
CC This is a AL-2-short (AL-2s) protein. The AL-2 is a novel Eph-related
CC tyrosine kinase receptor ligand. AL-2 can be administered to patients in
CC whom the nervous system has been damaged by trauma, surgery, stroke,
CC ischaemia, infection, metabolic disease, nutritional deficiency,
CC malignancy, or toxic agents, to promote the survival or growth of
CC neurons. They can be used to treat motoneuron disorders such as
CC amyotrophic lateral sclerosis (Lou Gehrig's disease), Bell's palsy, and
CC various conditions involving spinal muscular atrophy, or paralysis. AL-2
CC can be used to treat human neurodegenerative disorders, such as
CC Alzheimer's disease, Parkinson's disease, epilepsy, demyelinating
CC diseases such as multiple sclerosis, Huntingtons chorea, Down's syndrome,
CC nerve deafness, Menier's disease, and other disorders of the cerebellum.
CC AL-2 can be used as cognitive enhancer, to enhance learning particularly
CC in dementias or trauma, since they can promote axonal outgrowth and
CC synaptic plasticity, particularly of hippocampal neurons that express AL-
CC 2 binding Eph-family receptors and cortical neurons that express AL-2. AL
CC -2 can also be used for wound healing, i.e. accelerating
CC neovascularisation of, e.g. burns and ulcers. The encoding nucleic acids
CC are useful in preparing antibodies that specifically bind to the AL-2
CC protein. The antibodies and the AL-2 antagonists are useful in diagnosing
CC and treating various neuronal disorders. AL-2 antagonists can be used for
CC modulating angiogenesis. They can also be used for the treatment of
CC tumours, acute myeloid leukaemia (AML), chronic myeloid leukaemia (CML),
CC myelodysplastic syndrome (MDS), diabetic retinopathy, neovascular
CC glaucoma, psoriasis and rheumatoid arthritis
XX
SQ Sequence 340 AA;

Query Match 75.1%; Score 1841; DB 2; Length 340;
Best Local Similarity 100.0%; Pred. No. 2.4e-146;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

Qy         61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy        121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180

Qy        181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

Qy        241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300

Qy        301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
                ||||||||||||||||||||||||||||||||||||
Db        301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
```

```
RESULT 4
AAW10637
ID   AAW10637 standard; protein; 340 AA.
XX
AC   AAW10637;
XX
DT   23-JUN-1997  (first entry)
XX
DE   NLERK2 ligand for eph-related kinase.
XX
KW   LERK; ligand for eph-related kinase; ERK; NLERK2;
KW   receptor protein tyrosine kinase; cell proliferation;
KW   cell differentiation; cell survival; nerve cell.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .29
FT                   /label= Sig_peptide
FT   Protein         30. .340
FT                   /label= Mat_protein
FT   Modified-site   210
FT                   /label= N-glycosylation_site
FT   Domain          227. .251
FT                   /label= Transmembrane_domain
XX
PN   WO9704091-A1.
XX
PD   06-FEB-1997.
XX
PF   19-JUL-1996;   96WO-AU000460.
XX
PR   20-JUL-1995;   95AU-00004263.
PR   27-NOV-1995;   95AU-00006847.
PR   22-DEC-1995;   95AU-00007299.
PR   05-FEB-1996;   96AU-00007890.
XX
PA   (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
PI   Nicola NA;
XX
```

DR WPI; 1997-132632/12.
DR N-PSDB; AAT60966.
XX
PT Nucleic acid mol. encoding ligand for eph-related kinase - useful for
PT treatment of, pref. neuronal, cells to increase survival, proliferation
PT and differentiation.
XX
PS Claim 16; Page 37-39; 71pp; English.
XX
CC A novel human ligand for eph-related kinase (LERK) is designated NLERK2
CC (AAW10637). It is encoded by a cDNA clone (AAT60966) obtd. from a human
CC foetal brain cDNA library. The novel receptor ligand can be expressed in
CC transformed host cells and used in methods for regulating the
CC development, maintenance or regeneration of different cells (e.g.
CC neurons) and tissues in vivo and in vitro. Soluble NLERK2 peptides can be
CC used to treat injury, disease or abnormality in the nervous system, and
CC membrane-bound NLERK2 to modulate proliferation, different or survival
CC e.g. in grafting procedures or transplantation. NLERK2 can also be used
CC to raise antibodies for use in immunotherapy, and to detect anti-NLERK2
CC antibodies that may occur in some autoimmune diseases
XX
SQ Sequence 340 AA;

Query Match 75.1%; Score 1841; DB 2; Length 340;
Best Local Similarity 100.0%; Pred. No. 2.4e-146;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

Qy         61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy        121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180

Qy        181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

Qy        241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300

Qy        301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
              |||||||||||||||||||||||||||||||||||||
Db        301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
```

RESULT 5
ABU07845
ID ABU07845 standard; protein; 340 AA.
XX
AC ABU07845;

XX

DT 10-MAY-2003 (first entry)

XX

DE Human ephrin-B3 ligand.

XX

KW Cytostatic; vasodilator; antiinflammatory; cardiant; gene therapy;
KW ligand-receptor binding modulator; ephrin ligand; angiogenesis;
KW lymphangiogenesis; aberrant Ephrin-Tie biology; cell growth disorder;
KW cell migration disorder; cell proliferation disorder; neovascularisation;
KW ischaemia; infarction; tissue graft; transplant; human; ephrin-B3;
KW tie receptor tyrosine kinase; Eph receptor ligand.

XX

OS Homo sapiens.

XX

PN WO2003004529-A2.

XX

PD 16-JAN-2003.

XX

PF 02-JUL-2002; 2002WO-IB002524.

XX

PR 02-JUL-2001; 2001US-0302960P.

XX

PA (LICN) LICENTIA LTD.

XX

PI Alitalo K, Kubo H;

XX

DR WPI; 2003-210341/20.
DR N-PSDB; ABX12546.

XX

PT Identifying modulators of binding between a Tie receptor tyrosine kinase
PT and an Ephrin ligand, useful for promoting neovascularization, comprises
PT contacting a Tie receptor with an Ephrin in the presence of a putative
PT modulator.

XX

PS Disclosure; Page 117-119; 199pp; English.

XX

CC The invention describes a method of identifying a modulator of binding
CC between a Tie receptor tyrosine kinase and an Ephrin ligand. The method
CC comprises contacting a Tie receptor composition with an Ephrin
CC composition in the presence and in the absence of a putative modulator
CC compound, and detecting the binding between Tie receptor and the Ephrin
CC in the presence and in the absence of the putative modulator. The method
CC is useful for identifying a modulator of binding between a Tie receptor
CC tyrosine kinase and an Ephrin ligand. Modulators identified from the
CC method are useful in modulating angiogenic processes, including
CC lymphangiogenesis, for treating diseases associated with aberrant Ephrin-
CC Tie biology, aberrant growth, migration or proliferation of cells that
CC express a Tie receptor, or for promoting growth of vessel or
CC neovascularisation (e.g. ischaemic tissue, an infarction, a new or
CC chronic compound, or a tissue graft or transplant). This is the amino
CC acid sequence of human Ephrin-B3, a member of the Ephrin-B subclass of
CC ligands that are bound to the membrane via a transmembrane domain and
CC short cytoplasmic tail and function as Eph receptor ligands

XX

SQ Sequence 340 AA;

Query Match 75.1%; Score 1841; DB 6; Length 340;

```
  Best Local Similarity   100.0%;  Pred. No. 2.4e-146;
  Matches  338;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

Qy         61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy        121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180

Qy        181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

Qy        241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300

Qy        301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
              ||||||||||||||||||||||||||||||||||||||
Db        301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338


RESULT 6
AAW17081
ID   AAW17081 standard; protein; 340 AA.
XX
AC   AAW17081;
XX
DT   09-AUG-1997  (first entry)
XX
DE   EPH family ligand Efl-6.
XX
KW   Efl-6; Eph; Elk; receptor tyrosine kinase; signal transduction; ligand;
KW   neurological disease.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .24
FT                   /label= Sig_peptide
FT   Protein         25. .340
FT                   /label= Mat_protein
FT   Misc-difference 166
FT                   /label= Gln, Arg
FT   Domain          225. .249
FT                   /label= Transmembrane_domain
XX
PN   WO9715667-A1.
XX
PD   01-MAY-1997.
XX
```

PF 25-OCT-1996; 96WO-US017201.
XX
PR 25-OCT-1995; 95US-0007015P.
XX
PA (REGE-) REGENERON PHARM INC.
XX
PI Davis S, Gale NW, Yancopoulos GD;
XX
DR WPI; 1997-259021/23.
DR N-PSDB; AAT69808.
XX
PT New nucleic acid encoding Efl-6 ligand protein - used for promoting
PT growth and proliferation of neuronal cells and in drug screening.
XX
PS Claim 2; Fig 1; 36pp; English.
XX
CC A novel ligand (AAW17081), designated Efl-6 (or Eph transmembrane
CC tyrosine kinase family ligand 6), binds to the Elk, Nuk/Cek5, Hek2/Sek4,
CC Htk and Sek1 receptors on cells. Its amino acid sequence was deduced from
CC a human frontal cortex cDNA clone (AAT69808). Recombinant Elf-6,
CC truncated soluble polypeptides comprising the extracellular domain of Elf
CC -6, and Efl-6 ligandbodies comprising soluble Efl-6 and the Fc portion of
CC IgG can be expressed in host cells. These can be used to support neuronal
CC and other Eph receptor-bearing cell populations for treatment of
CC neurological disorders, in drug screening and to raise diagnostic
CC antibodies
XX
SQ Sequence 340 AA;

Query Match 74.9%; Score 1835; DB 2; Length 340;
Best Local Similarity 99.7%; Pred. No. 7.8e-146;
Matches 337; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

Qy         61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy        121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLXVGQSPRGGAVPRKP 180

Qy        181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

Qy        241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGGMGPREAEPGELGIALRGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGGMGPREAEPGELGIALRGG 300

Qy        301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
              ||||||||||||||||||||||||||||||||||||||
Db        301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
```

RESULT 7
AAW46615
ID AAW46615 standard; protein; 340 AA.
XX
AC AAW46615;
XX
DT 06-JUL-1998 (first entry)
XX
DE Human transmembrane ligand Elk-L3.
XX
KW Elk-L3; Elk-related receptor tyrosine kinase; transmembrane ligand;
KW human; signal transduction; axonogenesis; nerve cell; neurone;
KW Alzheimer's disease; Parkinson's disease; Huntingdon's disease;
KW demyelination; multiple sclerosis; amyotrophic lateral sclerosis;
KW nervous system infection; Wernicke's disease; trauma; ischaemia; stroke;
KW nutritional polyneuropathy; progressive supranuclear palsy;
KW Shy Drager's syndrome; multistem degeneration;
KW olivo ponto cerebellar atrophy, peripheral nerve damage.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT Misc-difference 166
FT   /label= Gln, Arg
FT Domain   225. .249
FT   /note= "transmembrane domain"
XX
PN WO9801548-A1.
XX
PD 15-JAN-1998.
XX
PF 04-JUL-1997; 97WO-CA000473.
XX
PR 05-JUL-1996; 96US-0021272P.
XX
PA (MOUN) MOUNT SINAI HOSPITAL CORP.
XX
PI Holland S, Mbamalu G, Pawson T;
XX
DR WPI; 1998-101047/09.
DR N-PSDB; AAV16097.
XX
PT Modulating transmembrane ligand for an Elk-related receptor tyrosine
PT kinase - by formation of a complex between an oligomerised Elk-related
PT receptor tyrosine kinase and a transmembrane ligand.
XX
PS Disclosure; Fig 5A; 40pp; English.
XX
CC This polypeptide comprises human Elk-L3, a transmembrane ligand of Elk-
CC related receptor tyrosine kinase (ERRTK). A novel method of modulating
CC the biological activity of, or for affecting a pathway regulated by, a
CC transmembrane ligand for an ERRTK in a cell expressing the transmembrane
CC ligand comprises forming a complex between a purified and isolated
CC oligomerised ERRTK, or an isoform or an extracellular domain of the
CC ERRTK, and the transmembrane ligand expressed on the cell. The complex
CC can also be used for evaluating a substance for its ability to modulate

CC the biological activity of a transmembrane ligand for an ERRTK, and to
CC identify substances that affect or modulate a pathway regulated by a
CC ERRTK. A purified and isolated oligomerised ERRTK can be used in the
CC preparation of a medicament for modulating neuronal development or
CC regeneration in a subject, or in a medicament for modulating axonogenesis
CC in a subject (all claimed). The substances identified by the methods can
CC be used to modulate axonogenesis, nerve cell interactions and
CC regeneration, to treat diseases and conditions involving trauma and
CC injury to the nervous system, such as Alzheimer's disease, Parkinson's
CC disease, Huntingdon's disease, demyelinating diseases, such as multiple
CC sclerosis, amyotrophic lateral sclerosis, bacterial and viral infections
CC of the nervous system, deficiency diseases, such as Wernicke's disease
CC and nutritional polyneuropathy, progressive supranuclear palsy, Shy
CC Drager's syndrome, multistem degeneration and olivo ponto cerebellar
CC atrophy, peripheral nerve damage, trauma, and ischaemia resulting from
CC stroke
XX
SQ Sequence 340 AA;

Query Match 74.6%; Score 1827; DB 2; Length 340;
Best Local Similarity 99.4%; Pred. No. 3.7e-145;
Matches 336; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

Qy         61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy        121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLXVGQSPRGGAVPRKP 180

Qy        181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

Qy        241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300

Qy        301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
              |||||||||||||||||||||||||||||| ||||
Db        301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPQNIYY 338
```

RESULT 8
ABU07846
ID ABU07846 standard; protein; 340 AA.
XX
AC ABU07846;
XX
DT 10-MAY-2003 (first entry)
XX
DE Mouse ephrin-B3 ligand.

XX
KW Cytostatic; vasodilator; antiinflammatory; cardiant; gene therapy;
KW ligand-receptor binding modulator; ephrin ligand; angiogenesis;
KW lymphangiogenesis; aberrant Ephrin-Tie biology; cell growth disorder;
KW cell migration disorder; cell proliferation disorder; neovascularisation;
KW ischaemia; infarction; tissue graft; transplant; mouse; ephrin-B3;
KW tie receptor tyrosine kinase; Eph receptor ligand.
XX
OS Mus musculus.
XX
PN WO2003004529-A2.
XX
PD 16-JAN-2003.
XX
PF 02-JUL-2002; 2002WO-IB002524.
XX
PR 02-JUL-2001; 2001US-0302960P.
XX
PA (LICN) LICENTIA LTD.
XX
PI Alitalo K, Kubo H;
XX
DR WPI; 2003-210341/20.
DR N-PSDB; ABX12547.
XX
PT Identifying modulators of binding between a Tie receptor tyrosine kinase
PT and an Ephrin ligand, useful for promoting neovascularization, comprises
PT contacting a Tie receptor with an Ephrin in the presence of a putative
PT modulator.
XX
PS Disclosure; Page 121-122; 199pp; English.
XX
CC The invention describes a method of identifying a modulator of binding
CC between a Tie receptor tyrosine kinase and an Ephrin ligand. The method
CC comprises contacting a Tie receptor composition with an Ephrin
CC composition in the presence and in the absence of a putative modulator
CC compound, and detecting the binding between Tie receptor and the Ephrin
CC in the presence and in the absence of the putative modulator. The method
CC is useful for identifying a modulator of binding between a Tie receptor
CC tyrosine kinase and an Ephrin ligand. Modulators identified from the
CC method are useful in modulating angiogenic processes, including
CC lymphangiogenesis, for treating diseases associated with aberrant Ephrin-
CC Tie biology, aberrant growth, migration or proliferation of cells that
CC express a Tie receptor, or for promoting growth of vessel or
CC neovascularisation (e.g. ischaemic tissue, an infarction, a new or
CC chronic compound, or a tissue graft or transplant). This is the amino
CC acid sequence of mouse Ephrin-B3, a member of the Ephrin-B subclass of
CC ligands that are bound to the membrane via a transmembrane domain and
CC short cytoplasmic tail and function as Eph receptor ligands
XX
SQ Sequence 340 AA;

Query Match 72.3%; Score 1771; DB 6; Length 340;
Best Local Similarity 95.6%; Pred. No. 1.9e-140;
Matches 323; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

```
                || ||  |||||:||||||||  ||||||||||||||||||||||||||||||||||||||||
Db           1 MGAPHFGPGGVQVGALLLLGFAGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

Qy          61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
                |||||||||||||||:||||||||  ||||||||||||||||||||||||||||||||||||
Db          61 LCPRARPPGPHSSPSYEFYKLYLVEGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy         121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180

Qy         181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
                |||||||||||||||  |||:: :||||:|||||||||||||||||||||||:|||||
Db         181 VSEMPMERDRGAAHSAEPGRDTIPGDPSSNATSRGAEGPLPPPSMPAVAGAAGGMALLLL 240

Qy         241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300

Qy         301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
                | ||||||||||||||||||||||||||||||||||
Db         301 GTADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
```

```
RESULT 9
AAW00287
ID   AAW00287 standard; protein; 334 AA.
XX
AC   AAW00287;
XX
DT   19-JAN-1997  (first entry)
XX
DE   Mouse Eph receptor ligand ELF-2.
XX
KW   Eph receptor; ligand; ELF-2; tyrosine kinase; signal transduction;
KW   organogenesis; oncogenesis; tumour; neurological disorder; diagnosis;
KW   gene therapy.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   Domain          1. .224
FT                   /label= Extracellular_domain
FT   Binding-site    31. .155
FT                   /label= Receptor_binding_site
FT   Domain          226. .251
FT                   /label= Transmembrane_domain
XX
PN   WO9626958-A2.
XX
PD   06-SEP-1996.
XX
PF   23-FEB-1996;   96WO-US002673.
XX
PR   27-FEB-1995;   95US-00395415.
XX
PA   (HARD ) HARVARD COLLEGE.
```

XX
PI Flanagan JG, Bergemann AD;
XX
DR WPI; 1996-433391/43.
DR N-PSDB; AAT40230.
XX
PT Eph receptor ligand, ELF-2, and DNA encoding it - used to treat or
PT prevent neurological diseases, and to modulate binding of ELF-2 to Eph
PT receptor, e.g. to prevent or treat tumour formation.
XX
PS Claim 6; Fig 1A-B; 50pp; English.
XX
CC Mouse Eph receptor ligand ELF-2 (AAW00287) is strongly expressed in the
CC anterior hindbrain and newly-forming somites of embryos at the early
CC organogenesis stage of development. It is important in cellular
CC communication during pattern formation. Its amino acid sequence was
CC deduced from a cDNA clone (AAT40230) isolated from a newborn mouse brain
CC cDNA library. The ELF-2 ligand can be used to alter neurological
CC development, oncogenesis and growth regulation, to modulate binding of
CC ELF-2 to the Eph receptor, and in diagnostic assays
XX
SQ Sequence 334 AA;

  Query Match   25.7%; Score 628.5; DB 2; Length 334;
  Best Local Similarity   41.8%; Pred. No. 2.4e-44;
  Matches 137; Conservative   49; Mismatches 129; Indels   13; Gaps   5;

```
Qy          14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
               | |::|    :   : |||:||||:| :|    | ||||||||:||::||:       :
Db          15 GLLMVLCRTAISRSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 71

Qy          74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
                 ||:||:|:|   |  ||        || | ||| |::||||||:|||||| ||: :
Db          72 GQYEYYKVYMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK 131

Qy         134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
               |||||:||:|: |||:: :|||| || ||:|::|||  |  | |    |     :|
Db         132 DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSARNHGPTRRPELEAGTN 191

Qy         191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
               | : :  |  :  ||  |   ::  :   |    :   || | |  : :: :      :
Db         192 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIIFIVIIITLVVLLL 251

Qy         251 WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
                 ||| :    :|    |     :   ||        :|| :: | ||    ||  ||||
Db         252 KYRRRHRKHSPQHTTTLSLSTLATPKRGGNN----NGSEPSDVIIPLR---TADSVFCPH 304

Qy         311 YEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
               ||||||||||||||: ||||| ||||
Db         305 YEKVSGDYGHPVYIVQEMPPQSPANIYY 332
```

RESULT 10
AAR92742
ID AAR92742 standard; protein; 336 AA.
XX
AC AAR92742;

XX
DT 21-MAY-1996 (first entry)
XX
DE Murine hepatoma transmembrane kinase receptor ligand.
XX
KW Hepatoma transmembrane kinase; Htk; receptor; ligand; tyrosine kinase;
KW neurodegenerative disease.
XX
OS Mus musculus.
XX
PN WO9602645-A2.
XX
PD 01-FEB-1996.
XX
PF 14-JUL-1995; 95WO-US008812.
XX
PR 20-JUL-1994; 94US-00277722.
XX
PA (GETH) GENENTECH INC.
XX
PI Bennett BD, Matthews W;
XX
DR WPI; 1996-105907/11.
DR N-PSDB; AAT16470.
XX
PT Ligand for the hepatoma trans-membrane kinase receptor - useful for
PT stimulating and inhibiting cells carrying the receptor, e.g. for treating
PT neuro-degenerative disease.
XX
PS Claim 5; Fig 1(A-D); 88pp; English.
XX
CC Mouse (AAT16470) and human (AAT16471) Htk ligand which bind to, and
CC activate, the Htk receptor, have been identified in a variety of tissues
CC using a soluble Htk-Fc fusion protein. The predicted mol.wt. of the
CC murine Htk ligand protein following a signal peptide cleavage is 34 kD
CC with an estimated pI of 8.9. The murine and human ligands show 96%
CC homology at the amino acid level. The DNA is used to produce recombinant
CC ligands; for tissue- specific typing (partic. as a marker for breast
CC cancer) and as a marker for human chromosome 13. The ligands (partic. in
CC soluble form) are used to activate the tyrosine kinase domain of the Htk
CC receptor, i.e. to stimulate or inhibit growth, differentiation, and/or
CC activation of cells contg. the receptor, e.g. treatment of
CC neurodegenerative diseases, since they are strongly expressed in the
CC cerebral cortex, hippocampus, striatum and cerebellum. The ligands are
CC also useful as a control or standard in assays, for generation of
CC antibodies, as a mol. wt. marker, for growth in vitro of Htk-receptor
CC positive cells, as research agent, in screening, etc
XX
SQ Sequence 336 AA;

Query Match 25.7%; Score 628.5; DB 2; Length 336;
Best Local Similarity 41.8%; Pred. No. 2.4e-44;
Matches 137; Conservative 49; Mismatches 129; Indels 13; Gaps 5;

```
Qy         14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
                | |::|    :   : |||:||||:| :|    | |||||||||:||::||:       :
Db         17 GLLMVLCRTAISRSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 73
```

```
Qy          74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
               ||:||:|:|   |  ||        || | ||| |::||||||||:|||||| ||: :
Db          74 GQYEYYKVYMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK 133

Qy         134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
               |||||:||:|: |||:: :|||| || ||:|::|||  |  | |    |     :|
Db         134 DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSARNHGPTRRPELEAGTN 193

Qy         191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
               | : :  |  :  ||  |   ::  :   |    :   || | |  : :: :      :
Db         194 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIIFIVIIITLVVLLL 253

Qy         251 WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
               |||  :    :|    |     :   ||        :|| :: | ||    ||  ||||
Db         254 KYRRRHRKHSPQHTTTLSLSTLATPKRGGNN----NGSEPSDVIIPLR---TADSVFCPH 306

Qy         311 YEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
               ||||||||||||||||: ||||| ||||
Db         307 YEKVSGDYGHPVYIVQEMPPQSPANIYY 334
```

RESULT 11
ABU07844
ID ABU07844 standard; protein; 336 AA.
XX
AC ABU07844;
XX
DT 10-MAY-2003 (first entry)
XX
DE Mouse ephrin-B2 ligand.
XX
KW Cytostatic; vasodilator; antiinflammatory; cardiant; gene therapy;
KW ligand-receptor binding modulator; ephrin ligand; angiogenesis;
KW lymphangiogenesis; aberrant Ephrin-Tie biology; cell growth disorder;
KW cell migration disorder; cell proliferation disorder; neovascularisation;
KW ischaemia; infarction; tissue graft; transplant; mouse; ephrin-B2;
KW tie receptor tyrosine kinase; Eph receptor ligand.
XX
OS Mus musculus.
XX
PN WO2003004529-A2.
XX
PD 16-JAN-2003.
XX
PF 02-JUL-2002; 2002WO-IB002524.
XX
PR 02-JUL-2001; 2001US-0302960P.
XX
PA (LICN) LICENTIA LTD.
XX
PI Alitalo K, Kubo H;
XX
DR WPI; 2003-210341/20.
DR N-PSDB; ABX12545.
XX
PT Identifying modulators of binding between a Tie receptor tyrosine kinase

PT and an Ephrin ligand, useful for promoting neovascularization, comprises
PT contacting a Tie receptor with an Ephrin in the presence of a putative
PT modulator.
XX
PS Example 1; Page 113-114; 199pp; English.
XX
CC The invention describes a method of identifying a modulator of binding
CC between a Tie receptor tyrosine kinase and an Ephrin ligand. The method
CC comprises contacting a Tie receptor composition with an Ephrin
CC composition in the presence and in the absence of a putative modulator
CC compound, and detecting the binding between Tie receptor and the Ephrin
CC in the presence and in the absence of the putative modulator. The method
CC is useful for identifying a modulator of binding between a Tie receptor
CC tyrosine kinase and an Ephrin ligand. Modulators identified from the
CC method are useful in modulating angiogenic processes, including
CC lymphangiogenesis, for treating diseases associated with aberrant Ephrin-
CC Tie biology, aberrant growth, migration or proliferation of cells that
CC express a Tie receptor, or for promoting growth of vessel or
CC neovascularisation (e.g. ischaemic tissue, an infarction, a new or
CC chronic compound, or a tissue graft or transplant). This is the amino
CC acid sequence of mouse Ephrin-B2, a member of the Ephrin-B subclass of
CC ligands that are bound to the membrane via a transmembrane domain and
CC short cytoplasmic tail and function as Eph receptor ligands
XX
SQ Sequence 336 AA;

Query Match 25.6%; Score 626.5; DB 6; Length 336;
Best Local Similarity 41.4%; Pred. No. 3.6e-44;
Matches 137; Conservative 49; Mismatches 126; Indels 19; Gaps 5;

```
Qy          14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
               | |::|    :   : |||:||||:| :|    | |||||||||:||::||:       :
Db          17 GLLMVLCRTAISRSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 73

Qy          74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
                 ||:||:|:|   |  ||        || | ||| |::||||||:|||||| ||: :
Db          74 GQYEYYKVYMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK 133

Qy         134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ------SPRGGAVPRKPVSEMPME 187
               |||||:||:|: |||:: :|||| || ||:|::|||      | |     |:|  |
Db         134 DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNHGPTRRPELE---A 190

Qy         188 RDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGG 247
                 | : :  |  :  ||  |   ::  :   |    :   || | |  : :: :
Db         191 GTNGRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIIFIVIIITLVV 250

Qy         248 AMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPF 307
                :  ||| :    :|    |     :   ||        :|| :: | ||    ||  |
Db         251 LLLKYRRRHRKHSPQHTTTLSLSTLATPKRGGNN----NGSEPSDVIIPLR---TADSVF 303

Qy         308 CPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
               ||||||||||||||||||: ||||| ||||
Db         304 CPHYEKVSGDYGHPVYIVQEMPPQSPANIYY 334
```

RESULT 12
AAR55059

```
ID   AAR55059 standard; protein; 346 AA.
XX
AC   AAR55059;
XX
DT   25-MAR-2003  (revised)
DT   28-JAN-1995  (first entry)
XX
DE   Elk tyrosine kinase receptor ligand.
XX
KW   Vectors; elk-L protein; elk; ligands; cell growth; differentiation.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .24
FT                   /note= "signal peptide"
FT   Protein         25. .346
FT                   /note= "mature elk-L protein"
XX
PN   WO9411384-A1.
XX
PD   26-MAY-1994.
XX
PF   15-NOV-1993;   93WO-US010955.
XX
PR   13-NOV-1992;   92US-00977693.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Lyman S,  Beckmann MP,  Baum PR;
XX
DR   WPI; 1994-183415/22.
DR   N-PSDB; AAQ65486.
XX
PT   New DNA encoding ligand for elk tyrosine kinase receptor - also related
PT   polypeptides, vectors, antibodies and probes, useful e.g. in studying
PT   cell differentiation or growth.
XX
PS   Claim 7; Page 30; 35pp; English.
XX
CC   The sequence is that of the elk-L protein able to bind elk, a tyrosine
CC   kinase receptor. The DNA may be incorporated into vectors which can used
CC   to study the role of elk and its ligands in cell growth and
CC   differentiation. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 346 AA;

  Query Match             25.4%;  Score 623;  DB 2;  Length 346;
  Best Local Similarity   39.2%;  Pred. No. 7.4e-44;
  Matches  143;  Conservative   48;  Mismatches  116;  Indels   58;  Gaps    9;

Qy          8 PGGVRVGALLLLGVLGLVSGL------SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
              ||   :|  |:  |:  :  |      :|||| |:| | :| :  | |:||:|||:||::
Db          4 PGQRWLGKWLVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63

Qy         62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
              ||||    |     ||:||||||   |   |     ||:|:||:||: ::|||||||:|
```

```
Db         64 CPRAEAGRP-----YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118

Qy        122 PNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
              ||  | ||: |||||| :||:|: |||| : |||| || ||::::||| |      :
Db        119 PNYMGLEFKKHHDYYITSTSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTT 178

Qy        182 SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
              |    | |     : : ||     ||      :   |    |       ||:|| :
Db        179 SRPSKEADNTVKMATQAPGSRGSLGDSDGKHETVNQEEKSGP-------GASGGSSGDPD 231

Qy        237 ------LLLLGVAGAGGA-------------MCWRRRRAKPSESRHPGPGSFGRGGSLGL 277
                    : |    |||               :  |:|  | ::          |  :| |
Db        232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLKLRKRHRKHTQQ---------RAAALSL 282

Qy        278 ----GGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
                  || |    || :: | ||     :  :||||||||||||||||||: |||||
Db        283 STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP 339

Qy        334 PNIYY 338
               ||||
Db        340 ANIYY 344
```

RESULT 13
AAR91930
ID AAR91930 standard; protein; 346 AA.
XX
AC AAR91930;
XX
DT 25-MAR-2003 (revised)
DT 11-DEC-1996 (first entry)
XX
DE Human cytokine elk-ligand (elk-L).
XX
KW Human; cytokine; elk-ligand; elk-L; tyrosine kinase receptor;
KW neurotrophic; neuroprotective; placenta; radiolabelled probe; treatment;
KW neural tissue; excito-toxicity; injury; disorder; neural culture reagent;
KW immunogenic fragment; antibody.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT Peptide   1. .24
FT   /label= sig_peptide
FT Peptide   25. .346
FT   /label= mat_peptide
XX
PN US5512457-A.
XX
PD 30-APR-1996.
XX
PF 15-MAR-1994; 94US-00213403.
XX
PR 13-NOV-1992; 92US-00977693.
XX
PA (IMMV) IMMUNEX CORP.
XX

PI Carpenter MK, Lyman S, Beckmann MP, Baum PR;
XX
DR WPI; 1996-229866/23.
DR N-PSDB; AAT28770.
XX
PT DNA coding for neurotrophic human elk ligand cytokine - useful as probe
PT to isolate other elk ligand sequences.
XX
PS Claim 1; Col 27-30; 18pp; English.
XX
CC The present sequence is the human cytokine elk-ligand (elk-L), which
CC binds a member of the tyrosine kinase receptor family. Elk-L exhibits
CC neurotrophic and neuroprotective properties, and has a calculated mol.
CC wt. 35180 daltons and a pI of 9.006. The elk-L cDNA, isolated from a
CC human placental cDNA library, can be radiolabelled and used as a probe
CC for isolating other mammalian elk-L cDNA. Elk-L can be used to treat
CC neural tissue disorders, partic. excito-toxicity associated injuries or
CC disorders, and as a neural culture reagent, while immunogenic fragments
CC of elk-L can be used to generate specific anti-elk-L antibodies. (Updated
CC on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 346 AA;

Query Match 25.4%; Score 623; DB 2; Length 346;
Best Local Similarity 39.2%; Pred. No. 7.4e-44;
Matches 143; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

```
Qy          8 PGGVRVGALLLLGVLGLVSGL------SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
              ||   :|  |:  |:  :  |      :|||| |:| | :| :  | |:||:|||:||:: 
Db          4 PGQRWLGKWLVAMVVWALCRLATPLAKNLEPVSWSSSLNPKFLSGKGLVIYPKIGDKLDII 63

Qy         62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
              ||||    |     ||:||||||   |   |     ||:|:||:||: ::|||||||:| 
Db         64 CPRAEAGRP-----YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118

Qy        122 PNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
              ||  | ||: |||||| :||:|: ||||: :|||| || ||::::||| |      :
Db        119 PNYMGLEFKKHHDYYITSTSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTT 178

Qy        182 SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
              |    | |     : : ||     ||      :   |    |       ||:|| :
Db        179 SRPSKEADNTVKMATQAPGSRGSLGDSDGKHETVNQEEKSGP-------GASGGSSGDPD 231

Qy        237 ------LLLLGVAGAGGA------------MCWRRRRAKPSESRHPGPGSFGRGGSLGL 277
                    : |    |||               :  |:|  | ::          |  :| |
Db        232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLKLRKRHRKHTQQ---------RAAALSL 282

Qy        278 ----GGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
                  || |    || :: | ||     :  :||||||||||||||||||: |||||
Db        283 STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP 339

Qy        334 PNIYY 338
               ||||
Db        340 ANIYY 344
```

RESULT 14

AAW19249
ID AAW19249 standard; protein; 346 AA.
XX
AC AAW19249;
XX
DT 25-MAR-2003 (revised)
DT 18-AUG-1997 (first entry)
XX
DE Human elk ligand protien.
XX
KW Human; elk; ligand; elk-L; cytokine; testing; measuring; purification;
KW neuroprotection; treatment; diabetic; hereditary; nutritional;
KW neuropathy; neurodegenerative disease; tissue culture.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT Peptide   1. .24
FT   /label= sig_peptide
FT Peptide   25. .346
FT   /label= mat_peptide
XX
PN US5627267-A.
XX
PD 06-MAY-1997.
XX
PF 01-JUN-1995; 95US-00458077.
XX
PR 13-NOV-1992; 92US-00977693.
PR 15-MAR-1994; 94US-00213403.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Beckmann MP, Lyman S, Baum PR;
XX
DR WPI; 1997-271366/24.
DR N-PSDB; AAT69766.
XX
PT Human elk ligand protein - for diagnostic or therapeutic use, e.g. as
PT neuro-protective agent.
XX
PS Claim 1; Col 29-32; 18pp; English.
XX
CC The present sequence is a human elk ligand (elk-L) protein, which binds
CC elk, has a calculated molecular weight of 35180 and an isoelectric point
CC of 9.006. Elk-L is a cytokine that can be used to test cells for elk
CC expression, measure the biological activity of elk, purify elk by
CC affinity chromatography and as a neuroprotective agent to treat diabetic,
CC hereditary and nutritional neuropathies and neurodegenerative diseases.
CC It may also be added to tissue cultures to prolong the life of neurons.
CC The elk-L cDNA was isolated from a human placental cDNA library, and is
CC present as a cDNA insert in the recombinant vector deposited in strain
CC ATCC 69085. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 346 AA;

Query Match 25.4%; Score 623; DB 2; Length 346;

```
  Best Local Similarity   39.2%;  Pred. No. 7.4e-44;
  Matches  143;  Conservative   48;  Mismatches  116;  Indels   58;  Gaps    9;

Qy          8 PGGVRVGALLLLGVLGLVSGL------SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
              ||   :|  |:  |:  :  |      :|||| |:| | :| :  | |:||:|||:||:: 
Db          4 PGQRWLGKWLVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63

Qy         62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
              ||||    |     ||:|||||   |   |     ||:|:||:||: ::|||||||:| 
Db         64 CPRAEAGRP-----YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118

Qy        122 PNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
              ||  | ||: |||||| :||:|: |||| : |||| || ||::::||| |       : 
Db        119 PNYMGLEFKKHHDYYITSTSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTT 178

Qy        182 SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
              |    | |     : : ||     ||      :   |    |       ||:|| :    
Db        179 SRPSKEADNTVKMATQAPGSRGSLGDSDGKHETVNQEEKSGP-------GASGGSSGDPD 231

Qy        237 ------LLLLGVAGAGGA-------------MCWRRRRAKPSESRHPGPGSFGRGGSLGL 277
                   : |    |||               :  |:|  | ::          |  :| | 
Db        232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLKLRKRHRKHTQQ---------RAAALSL 282

Qy        278 ----GGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
                  || |    || :: | ||     :  :|||||||||||||||||||: |||||
Db        283 STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP 339

Qy        334 PNIYY 338
               ||||
Db        340 ANIYY 344
```

```
RESULT 15
AAW36055
ID   AAW36055 standard; protein; 346 AA.
XX
AC   AAW36055;
XX
DT   06-MAR-1998  (first entry)
XX
DE   Human elk-L protein.
XX
KW   Human; elk-L; cytokine; ligand; tyrosine kinase receptor; fusion protein;
KW   extracellular domain; immunoglobulin; neurological disease.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .24
FT                   /note= "signal peptide"
FT   Protein         25. .346
FT                   /note= "mature protein"
FT   Domain          25. .237
FT                   /note= "extracellular domain; this region is used to
FT                   generate a fusion protein with the Fc portion of the
FT                   human immunoglobulin G1"
FT   Modified-site   139. .141
```

```
FT                   /note= "Asn is N-glycosylated"
FT   Domain          238. .265
FT                   /note= "transmembrane domain"
FT   Domain          266. .346
FT                   /note= "intracellular domain"
FT   Cleavage-site   266. .267
FT                   /note= "KEX2 protease cleavage site"
FT   Cleavage-site   267. .268
FT                   /note= "KEX2 protease cleavage site"
FT   Cleavage-site   270. .271
FT                   /note= "KEX2 protease cleavage site"
XX
PN   US5670625-A.
XX
PD   23-SEP-1997.
XX
PF   02-JUN-1995;   95US-00460741.
XX
PR   13-NOV-1992;   92US-00977693.
PR   15-MAR-1994;   94US-00213403.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Beckmann MP,  Lyman S,  Baum PR;
XX
DR   WPI; 1997-479524/44.
DR   N-PSDB; AAT97976.
XX
PT   Soluble fusion proteins of human elk-ligand and Fc immunoglobulin
PT   fragment - and their dimers and oligomers, useful as neuro-protectants
PT   and neurotrophic agents.
XX
PS   Claim 1; Col 27-30; 18pp; English.
XX
CC   This is the amino acid sequence of the human elk-L protein, a new
CC   cytokine that is the ligand for the elk tyrosine kinase receptor. The
CC   extracellular domain of the protein (amino acids 1-213) is used to
CC   generate a fusion protein comprising the Fc polypeptide of the human
CC   immunoglobulin G1 (extending from the hinge region to the C-terminus).
CC   The fusion protein (which has the same activities as the natural elk-L
CC   protein) has neuroprotective and neurotrophic activity so is potentially
CC   useful for treating a wide range of neurological diseases
XX
SQ   Sequence 346 AA;
```

```
  Query Match             25.4%;  Score 623;  DB 2;  Length 346;
  Best Local Similarity   39.2%;  Pred. No. 7.4e-44;
  Matches  143;  Conservative   48;  Mismatches  116;  Indels   58;  Gaps    9;

Qy          8 PGGVRVGALLLLGVLGLVSGL------SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
              ||   :|  |:  |:  :  |      :|||| |:| | :| :  | |:||:|||:||::
Db          4 PGQRWLGKWLVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63

Qy         62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
              ||||    |     ||:||||||   |   |     ||:|:||:||: ::|||||||:|
Db         64 CPRAEAGRP-----YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118
```

```
Qy        122 PNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
              ||  | ||: |||||| :|||:|: |||| : |||| || ||::::||| |      :
Db        119 PNYMGLEFKKHHDYYITSTSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTT 178

Qy        182 SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
              |    | |     : : ||     ||      :   |    |       ||:|| :
Db        179 SRPSKEADNTVKMATQAPGSRGSLGDSDGKHETVNQEEKSGP-------GASGGSSGDPD 231

Qy        237 ------LLLLGVAGAGGA-------------MCWRRRRAKPSESRHPGPGSFGRGGSLGL 277
                    : |    |||               :  |:|  | ::          |  :| |
Db        232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLKLRKRHRKHTQQ---------RAAALSL 282

Qy        278 ----GGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
                     || |    || :: | ||     :  :||||||||||||||||||: |||||
Db        283 STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP 339

Qy        334 PNIYY 338
               ||||
Db        340 ANIYY 344
```

Search completed: April 13, 2004, 09:24:15
Job time : 61.3774 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 13, 2004, 09:22:18 ; Search time 32.6226 Seconds
(without alignments)
720.046 Million cell updates/sec

Title: US-10-021-121-2
Perfect score: 2450
Sequence: 1 MGPPHSGPGGVRVGALLLLG.....TTLLRQRASVEAEAGQHGPL 455

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1837	75.0	340	4	US-09-214-631-3	Sequence 3, Appli
2	1835	74.9	340	4	US-09-051-994-2	Sequence 2, Appli
3	628.5	25.7	336	1	US-08-436-044-2	Sequence 2, Appli
4	628.5	25.7	336	2	US-08-436-054-2	Sequence 2, Appli
5	628.5	25.7	336	5	PCT-US95-08812-2	Sequence 2, Appli
6	623	25.4	346	1	US-08-213-403-2	Sequence 2, Appli
7	623	25.4	346	1	US-08-458-077-2	Sequence 2, Appli
8	623	25.4	346	1	US-08-460-741-2	Sequence 2, Appli
9	623	25.4	346	1	US-08-747-240-2	Sequence 2, Appli
10	623	25.4	346	1	US-08-299-567-6	Sequence 6, Appli
11	623	25.4	346	4	US-09-039-642B-2	Sequence 2, Appli

12	620.5	25.3	333	1	US-08-436-044-4	Sequence 4, Appli
13	620.5	25.3	333	2	US-08-436-054-4	Sequence 4, Appli
14	620.5	25.3	333	4	US-08-271-948-2	Sequence 2, Appli
15	620.5	25.3	333	4	US-08-739-333-2	Sequence 2, Appli
16	620.5	25.3	333	4	US-09-754-105-2	Sequence 2, Appli
17	620.5	25.3	333	4	US-09-978-339-2	Sequence 2, Appli
18	620.5	25.3	333	5	PCT-US95-08534-2	Sequence 2, Appli
19	620.5	25.3	333	5	PCT-US95-08812-4	Sequence 4, Appli
20	613.5	25.0	333	4	US-09-214-631-4	Sequence 4, Appli
21	599.5	24.5	345	4	US-09-214-631-5	Sequence 5, Appli
22	489	20.0	89	4	US-09-214-631-13	Sequence 13, Appl
23	192	7.8	82	4	US-09-214-631-11	Sequence 11, Appl
24	191.5	7.8	82	4	US-09-214-631-12	Sequence 12, Appl
25	179	7.3	234	1	US-08-299-567-5	Sequence 5, Appli
26	179	7.3	238	1	US-08-240-124-2	Sequence 2, Appli
27	179	7.3	238	1	US-08-453-943-2	Sequence 2, Appli
28	179	7.3	238	2	US-09-057-121-2	Sequence 2, Appli
29	179	7.3	238	3	US-09-358-734-2	Sequence 2, Appli
30	176.5	7.2	135	1	US-08-299-567-7	Sequence 7, Appli
31	176	7.2	184	1	US-09-609-324A-2	Sequence 2, Appli
32	176	7.2	184	2	US-08-920-440B-2	Sequence 2, Appli
33	176	7.2	184	3	US-09-173-492-2	Sequence 2, Appli
34	176	7.2	184	3	US-09-173-133-2	Sequence 2, Appli
35	176	7.2	184	3	US-09-165-533-2	Sequence 2, Appli
36	176	7.2	184	4	US-09-580-236A-2	Sequence 2, Appli
37	176	7.2	184	5	PCT-US95-12779-2	Sequence 2, Appli
38	176	7.2	184	5	PCT-US95-15781-2	Sequence 2, Appli
39	176	7.2	209	1	US-08-455-001-2	Sequence 2, Appli
40	176	7.2	209	3	US-08-308-814-2	Sequence 2, Appli
41	176	7.2	209	5	PCT-US95-11869-2	Sequence 2, Appli
42	175.5	7.2	213	1	US-09-609-324A-10	Sequence 10, Appl
43	175.5	7.2	213	2	US-08-920-440B-10	Sequence 10, Appl
44	175.5	7.2	213	3	US-09-173-492-10	Sequence 10, Appl
45	175.5	7.2	213	3	US-09-173-133-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-214-631-3
; Sequence 3, Application US/09214631
; Patent No. 6413730
; GENERAL INFORMATION:
; APPLICANT: Holland, Sacha
; APPLICANT: Mbamalu, Geraldine
; APPLICANT: Pawson, Tony
; TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
; TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
; TITLE OF INVENTION: TYROSINE KINASES
; FILE REFERENCE: 11757.23USWO
; CURRENT APPLICATION NUMBER: US/09/214,631
; CURRENT FILING DATE: 1999-03-12
; EARLIER APPLICATION NUMBER: PCT/CA97/00473
; EARLIER FILING DATE: 1997-07-04
; EARLIER APPLICATION NUMBER: 60/021,272
; EARLIER FILING DATE: 1996-07-05

```
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 340
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-214-631-3

  Query Match             75.0%;  Score 1837;  DB 4;  Length 340;
  Best Local Similarity   99.7%;  Pred. No. 4.3e-146;
  Matches  337;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

Qy         61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy        121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
              ||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||
Db        121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLQVGQSPRGGAVPRKP 180

Qy        181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

Qy        241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300

Qy        301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
              ||||||||||||||||||||||||||||||||||||||
Db        301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338


RESULT 2
US-09-051-994-2
; Sequence 2, Application US/09051994A
; Patent No. 6602683
; GENERAL INFORMATION:
;  APPLICANT: REGENERON PHARMACEUTICALS, INC.
;  TITLE OF INVENTION: BIOLOGICALLY ACTIVE EPH FAMILY LIGANDS
;  FILE REFERENCE: REG-341-PCT-US
;  CURRENT APPLICATION NUMBER: US/09/051,994A
;  CURRENT FILING DATE: 1998-04-24
;  EARLIER APPLICATION NUMBER: PCT/US96/17201
;  EARLIER FILING DATE: 1996-10-25
;  EARLIER APPLICATION NUMBER: 60/007,015
;  EARLIER FILING DATE: 1995-10-25
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 340
;   TYPE: PRT
;   ORGANISM: Homo sapiens
```

```
;   FEATURE:
;   NAME/KEY: site
;   LOCATION: (166)
;   OTHER INFORMATION: Xaa=Arg or Gln
US-09-051-994-2

  Query Match             74.9%;  Score 1835;  DB 4;  Length 340;
  Best Local Similarity   99.7%;  Pred. No. 6.4e-146;
  Matches  337;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

Qy         61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy        121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLXVGQSPRGGAVPRKP 180

Qy        181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

Qy        241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300

Qy        301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
              ||||||||||||||||||||||||||||||||||||||
Db        301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338


RESULT 3
US-08-436-044-2
; Sequence 2, Application US/08436044
; Patent No. 5624899
;  GENERAL INFORMATION:
;    APPLICANT:  Bennett, Brian D.
;    APPLICANT:  Matthews, William
;    TITLE OF INVENTION:  HTK LIGAND
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
```

```
;       APPLICATION NUMBER:  US/08/436,044
;       FILING DATE:  05-MAY-1995
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/277722
;       FILING DATE:  20-JUL-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Lee, Wendy M.
;       REGISTRATION NUMBER:  00,000
;       REFERENCE/DOCKET NUMBER:  902D3
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415/225-1994
;       TELEFAX:  415/952-9881
;       TELEX:  910/371-7168
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  336 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
US-08-436-044-2

  Query Match             25.7%;  Score 628.5;  DB 1;  Length 336;
  Best Local Similarity   41.8%;  Pred. No. 8.2e-45;
  Matches  137;  Conservative   49;  Mismatches  129;  Indels   13;  Gaps    5;

Qy          14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
               | |::|    :   : |||:||||:| :|    | |||||||||:||::||:       :
Db          17 GLLMVLCRTAISRSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 73

Qy          74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
                 ||:||:|:|   |  ||        || | ||| |::||||||:|||||| ||: :
Db          74 GQYEYYKVYMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK 133

Qy         134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
               |||||:||:|: |||:: :|||| || ||:|::|||  |  | |    |     :|
Db         134 DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSARNHGPTRRPELEAGTN 193

Qy         191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
               | : :  |  :  ||  |   ::  :   |    :   || | |  : :: :      :
Db         194 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIIFIVIIITLVVLLL 253

Qy         251 WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
                 ||| :    :|    |     :   ||        :|| :: | ||    ||  ||||
Db         254 KYRRRHRKHSPQHTTTLSLSTLATPKRGGNN----NGSEPSDVIIPLR---TADSVFCPH 306

Qy         311 YEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
               |||||||||||||||: ||||| ||||
Db         307 YEKVSGDYGHPVYIVQEMPPQSPANIYY 334


RESULT 4
US-08-436-054-2
; Sequence 2, Application US/08436054
; Patent No. 5864020
;  GENERAL INFORMATION:
;    APPLICANT:  Bennett, Brian D.
;    APPLICANT:  Matthews, William
```

```
;    TITLE OF INVENTION:  HTK LIGAND
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/436,054
;      FILING DATE:  05-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/277722
;      FILING DATE:  20-JUL-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lee, Wendy M.
;      REGISTRATION NUMBER:  00,000
;      REFERENCE/DOCKET NUMBER:  902D1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-1994
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  336 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-436-054-2

  Query Match             25.7%;  Score 628.5;  DB 2;  Length 336;
  Best Local Similarity   41.8%;  Pred. No. 8.2e-45;
  Matches  137;  Conservative   49;  Mismatches  129;  Indels   13;  Gaps    5;

Qy         14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
              | |::|    :   : |||:||||:| :|    | ||||||||:||::||:       :
Db         17 GLLMVLCRTAISRSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 73

Qy         74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
                ||:||:|:|   |  ||        || | ||| |::||||||:|||||| ||: :
Db         74 GQYEYYKVYMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK 133

Qy        134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
              |||||:||:|: |||:: :|||| || ||:|::|||  |  | |    |     :|
Db        134 DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSARNHGPTRRPELEAGTN 193

Qy        191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
              | : :  |  :  ||  |   ::  :   |    :   || | |  : :: :      :
Db        194 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIIFIVIIITLVVLLL 253

Qy        251 WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
```

```
                ||| :    :|    |     :   ||        :|| :: | ||    ||  ||||
Db        254 KYRRRHRKHSPQHTTTLSLSTLATPKRGGNN----NGSEPSDVIIPLR---TADSVFCPH 306

Qy        311 YEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
              ||||||||||||||||: ||||| ||||
Db        307 YEKVSGDYGHPVYIVQEMPPQSPANIYY 334


RESULT 5
PCT-US95-08812-2
; Sequence 2, Application PC/TUS9508812
;  GENERAL INFORMATION:
;    APPLICANT:  Genentech, Inc.
;    TITLE OF INVENTION:  HTK LIGAND
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/08812
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lee, Wendy M.
;      REGISTRATION NUMBER:  00,000
;      REFERENCE/DOCKET NUMBER:  902PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-1994
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  336 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
PCT-US95-08812-2

  Query Match             25.7%;  Score 628.5;  DB 5;  Length 336;
  Best Local Similarity   41.8%;  Pred. No. 8.2e-45;
  Matches  137;  Conservative   49;  Mismatches  129;  Indels   13;  Gaps    5;

Qy         14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
              | |::|    :   : |||:||||:| :|    | |||||||:||::||:       :
Db         17 GLLMVLCRTAISRSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 73
```

```
Qy         74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
              ||:||:|:|   |  ||        || | ||| |::|||||||:|||||| ||: :
Db         74 GQYEYYKVYMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK 133

Qy        134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
              |||||:||:|: |||:: :|||| || ||:|::|||  |  | |    |     :|
Db        134 DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSARNHGPTRRPELEAGTN 193

Qy        191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
              | : :  |  :  ||  |   ::  :   |    :   || | |  : :: :      :
Db        194 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIIFIVIIITLVVLLL 253

Qy        251 WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
              |||  :    :|    |     :   ||        :|| :: | ||    ||  ||||
Db        254 KYRRRHRKHSPQHTTTLSLSTLATPKRGGNN----NGSEPSDVIIPLR---TADSVFCPH 306

Qy        311 YEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
              ||||||||||||||: ||||| ||||
Db        307 YEKVSGDYGHPVYIVQEMPPQSPANIYY 334
```

```
RESULT 6
US-08-213-403-2
; Sequence 2, Application US/08213403
; Patent No. 5512457
;  GENERAL INFORMATION:
;    APPLICANT:  Lyman, Stewart D.
;    APPLICANT:  Beckmann, M. Patricia
;    APPLICANT:  Baum, Peter R
;    APPLICANT:  Carpenter, Melissa
;    TITLE OF INVENTION:  No. 5512457el Cytokine Designated elk Ligand
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Apple System 7.1
;      SOFTWARE:  Microsoft Word for Apple, Version 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/213,403
;      FILING DATE:  15-MAR-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/977,693
;      FILING DATE:  13-NOV-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seese, Kathryn A.
;      REGISTRATION NUMBER:  32,172
;      REFERENCE/DOCKET NUMBER:  2807-A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 587-0430
```

```
;      TELEFAX:  (206) 233-0644
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  346 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-213-403-2

  Query Match             25.4%;  Score 623;  DB 1;  Length 346;
  Best Local Similarity   39.2%;  Pred. No. 2.5e-44;
  Matches  143;  Conservative   48;  Mismatches  116;  Indels   58;  Gaps    9;

Qy          8 PGGVRVGALLLLGVLGLVSGL------SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
              ||   :|  |:  |:  :  |      :|||| |:| | :| :  | |:||:|||:||:: 
Db          4 PGQRWLGKWLVAMVVWALCRLATPLAKNLEPVSWSSSLNPKFLSGKGLVIYPKIGDKLDII 63

Qy         62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
              ||||    |     ||:||||||   |   |     ||:|:||:||: ::|||||||:| 
Db         64 CPRAEAGRP-----YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118

Qy        122 PNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
              ||  | ||: |||||| :||:|: ||||: :|||| || ||::::||| |      :
Db        119 PNYMGLEFKKHHDYYITSTSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTT 178

Qy        182 SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
              |    | |     : : ||     ||      :   |    |       ||:|| :
Db        179 SRPSKEADNTVKMATQAPGSRGSLGDSDGKHETVNQEEKSGP-------GASGGSSGDPD 231

Qy        237 ------LLLLGVAGAGGA-------------MCWRRRRAKPSESRHPGPGSFGRGGSLGL 277
                    : |    |||               :  |:|  | ::          |  :| |
Db        232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLKLRKRHRKHTQQ---------RAAALSL 282

Qy        278 ----GGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
                  || |    || :: | ||     :  :|||||||||||||||||||: |||||
Db        283 STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP 339

Qy        334 PNIYY 338
               ||||
Db        340 ANIYY 344


RESULT 7
US-08-458-077-2
; Sequence 2, Application US/08458077
; Patent No. 5627267
;  GENERAL INFORMATION:
;    APPLICANT:  Lyman, Stewart D.
;    APPLICANT:  Beckmann, M. Patricia
;    APPLICANT:  Baum, Peter R
;    APPLICANT:  Carpenter, Melissa
;    TITLE OF INVENTION:  No. 5627267el Cytokine Designated elk Ligand
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
```

; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple System 7.1
; SOFTWARE: Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,077
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/213,403
; FILING DATE: 15-MAR-1994
; APPLICATION NUMBER: US 07/977,693
; FILING DATE: 13-NOV-1992
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2807-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 346 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-458-077-2

Query Match 25.4%; Score 623; DB 1; Length 346;
Best Local Similarity 39.2%; Pred. No. 2.5e-44;
Matches 143; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

```
Qy          8 PGGVRVGALLLLGVLGLVSGL------SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
              ||   :|  |:  |:  :  |      :|||| |:| | :| :  | |:||:|||:||::
Db          4 PGQRWLGKWLVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63

Qy         62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
              ||||    |     ||:||||||   |   |     ||:|:|||:||: ::|||||||:|
Db         64 CPRAEAGRP-----YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118

Qy        122 PNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
              ||  | ||: ||||||  :||:|: ||||: :|||| || ||::::||| |      :
Db        119 PNYMGLEFKKHHDYYITSTSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTT 178

Qy        182 SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
              |    | |     : : ||     ||      :   |    |       ||:|| :
Db        179 SRPSKEADNTVKMATQAPGSRGSLGDSDGKHETVNQEEKSGP-------GASGGSSGDPD 231

Qy        237 ------LLLLGVAGAGGA------------MCWRRRRAKPSESRHPGPGSFGRGGSLGL 277
                    : |    |||               :  |:|  | ::          |  :| |
Db        232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLKLRKRHRKHTQQ---------RAAALSL 282
```

```
Qy        278 ----GGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
                  || |    || :: | ||     :  :||||||||||||||||||: |||||
Db        283 STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP 339

Qy        334 PNIYY 338
               ||||
Db        340 ANIYY 344
```

RESULT 8
US-08-460-741-2
; Sequence 2, Application US/08460741
; Patent No. 5670625
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; APPLICANT: Baum, Peter R
; APPLICANT: Carpenter, Melissa
; TITLE OF INVENTION: No. 5670625el Cytokine Designated elk Ligand
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple System 7.1
; SOFTWARE: Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,741
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/213,403
; FILING DATE: 15-MAR-1994
; APPLICATION NUMBER: US 07/977,693
; FILING DATE: 13-NOV-1992
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2807-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 346 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-460-741-2

```
  Query Match             25.4%;  Score 623;  DB 1;  Length 346;
  Best Local Similarity   39.2%;  Pred. No. 2.5e-44;
  Matches  143;  Conservative   48;  Mismatches  116;  Indels   58;  Gaps    9;

Qy          8 PGGVRVGALLLLGVLGLVSGL------SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
              ||   :|  |:  |:  :  |      :|||| |:| | :| :  | |:||:|||:||:: 
Db          4 PGQRWLGKWLVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63

Qy         62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
              ||||    |     ||:||||||   |   |     ||:|:||:||: ::|||||||:| 
Db         64 CPRAEAGRP-----YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118

Qy        122 PNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
              ||  | ||: |||||| :||:|: |||| : :|||| || ||::::||| |      : 
Db        119 PNYMGLEFKKHHDYYITSTSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTT 178

Qy        182 SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
              |    | |     : : ||     ||      :   |    |       ||:|| :    
Db        179 SRPSKEADNTVKMATQAPGSRGSLGDSDGKHETVNQEEKSGP-------GASGGSSGDPD 231

Qy        237 ------LLLLGVAGAGGA-------------MCWRRRRAKPSESRHPGPGSFGRGGSLGL 277
                   : |    |||                :  |:|  | ::          |  :| | 
Db        232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLKLRKRHRKHTQQ---------RAAALSL 282

Qy        278 ----GGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
                  || |    || :: | ||     :  :||||||||||||||||||: |||||
Db        283 STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP 339

Qy        334 PNIYY 338
               ||||
Db        340 ANIYY 344


RESULT 9
US-08-747-240-2
; Sequence 2, Application US/08747240
; Patent No. 5728813
;  GENERAL INFORMATION:
;    APPLICANT:  Lyman, Stewart D.
;    APPLICANT:  Beckmann, M. Patricia
;    APPLICANT:  Baum, Peter R
;    APPLICANT:  Carpenter, Melissa
;    TITLE OF INVENTION:  No. 5728813el Cytokine Designated elk Ligand
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Apple System 7.1
;      SOFTWARE:  Microsoft Word for Apple, Version 5.1a
;    CURRENT APPLICATION DATA:
```

; APPLICATION NUMBER: US/08/747,240
; FILING DATE: 12-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/213,403
; FILING DATE: 15-MAR-1994
; APPLICATION NUMBER: US 07/977,693
; FILING DATE: 13-NOV-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2807-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 346 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-747-240-2

Query Match 25.4%; Score 623; DB 1; Length 346;
Best Local Similarity 39.2%; Pred. No. 2.5e-44;
Matches 143; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

```
Qy          8 PGGVRVGALLLLGVLGLVSGL------SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
              ||   :|  |:  |:  :  |      :|||| |:| | :| :  | |:||:|||:||:: 
Db          4 PGQRWLGKWLVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63

Qy         62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
              ||||    |     ||:||||||   |   |     ||:|:||:||: ::|||||||:| 
Db         64 CPRAEAGRP-----YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118

Qy        122 PNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
              ||  | ||: |||||| :||:|: |||||: :|||| || ||::::||| |      : 
Db        119 PNYMGLEFKKHHDYYITSTSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTT 178

Qy        182 SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
              |    | |     : : ||     ||      :   |    |       ||:|| :     
Db        179 SRPSKEADNTVKMATQAPGSRGSLGDSDGKHETVNQEEKSGP-------GASGGSSGDPD 231

Qy        237 ------LLLLGVAGAGGA-------------MCWRRRRAKPSESRHPGPGSFGRGGSLGL 277
                    : |    |||               :  |:|  | ::          |  :| | 
Db        232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLKLRKRHRKHTQQ---------RAAALSL 282

Qy        278 ----GGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
                   || |    || :: | ||     :  :|||||||||||||||||||: |||||  
Db        283 STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP 339

Qy        334 PNIYY 338
               ||||
Db        340 ANIYY 344
```

```
RESULT 10
US-08-299-567-6
; Sequence 6, Application US/08299567
; Patent No. 5747033
;  GENERAL INFORMATION:
;    APPLICANT:  Davis, et al.
;    TITLE OF INVENTION:  METHOD OF ENHANCING THE BIOLOGICAL
;    TITLE OF INVENTION:  ACTIVITY OF EPH FAMILY LIGANDS
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Regeneron Pharmaceuticals, Inc.
;      STREET:  777 Old Saw Mill River Road
;      CITY:  Tarrytown
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10591-6707
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/299,567
;      FILING DATE:  01-SEP-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kempler, Gail M.
;      REGISTRATION NUMBER:  32,143
;      REFERENCE/DOCKET NUMBER:  REG 290
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  914-345-7400
;      TELEFAX:  914-345-7721
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  346 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
US-08-299-567-6

  Query Match             25.4%;  Score 623;  DB 1;  Length 346;
  Best Local Similarity   39.2%;  Pred. No. 2.5e-44;
  Matches  143;  Conservative   48;  Mismatches  116;  Indels   58;  Gaps    9;

Qy          8 PGGVRVGALLLLGVLGLVSGL------SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
              ||   :|  |:  |:  :  |      :|||| |:| | :| :  | |:||:|||:||::
Db          4 PGQRWLGKWLVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63

Qy         62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
              ||||    |     ||:||||||   |   |     ||:|:||:||: ::|||||||||:|
Db         64 CPRAEAGRP-----YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118

Qy        122 PNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
              ||  | ||: ||||||  :||:|: ||||: :|||| || ||::::||| |      :
Db        119 PNYMGLEFKKHHDYYITSTSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTT 178
```

```
Qy        182 SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
              |    | |     : : ||     ||      :   |    |       ||:|| :
Db        179 SRPSKEADNTVKMATQAPGSRGSLGDSDGKHETVNQEEKSGP-------GASGGSSGDPD 231

Qy        237 ------LLLLGVAGAGGA-------------MCWRRRRAKPSESRHPGPGSFGRGGSLGL 277
                    : |    |||               :  |:|  | ::          |  :| |
Db        232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLKLRKRHRKHTQQ---------RAAALSL 282

Qy        278 ----GGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
                  || |    || :: | ||     :  :||||||||||||||||||: |||||
Db        283 STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP 339

Qy        334 PNIYY 338
              ||||
Db        340 ANIYY 344
```

RESULT 11
US-09-039-642B-2
; Sequence 2, Application US/09039642B
; Patent No. 6540992
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; APPLICANT: Baum, Peter R.
; APPLICANT: Carpenter, Melissa K.
; TITLE OF INVENTION: NOVEL CYTOKINE DESIGNATED ELK LIGAND
; FILE REFERENCE: GENENT.67CPDV3
; CURRENT APPLICATION NUMBER: US/09/039,642B
; CURRENT FILING DATE: 1998-03-16
; PRIOR APPLICATION NUMBER: 08/213,403
; PRIOR FILING DATE: 1994-03-15
; PRIOR APPLICATION NUMBER: 07/977,693
; PRIOR FILING DATE: 1992-11-13
; PRIOR APPLICATION NUMBER: 08/747,240
; PRIOR FILING DATE: 1996-10-12
; PRIOR APPLICATION NUMBER: 08/460,741
; PRIOR FILING DATE: 1995-06-02
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 346
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-039-642B-2

  Query Match   25.4%; Score 623; DB 4; Length 346;
  Best Local Similarity   39.2%; Pred. No. 2.5e-44;
  Matches 143; Conservative   48; Mismatches 116; Indels   58; Gaps   9;

```
Qy          8 PGGVRVGALLLLGVLGLVSGL------SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
              ||   :|  |:  |:  :  |      :|||| |:| | :| :  | |:||:|||:||::
Db          4 PGQRWLGKWLVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63

Qy         62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
              ||||    |     ||:||||||   |   |     ||:|:||:||: ::|||||||:|
Db         64 CPRAEAGRP-----YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118
```

```
Qy        122 PNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
              ||  | ||: |||||| :||:|: |||||: :|||| || ||:::::||| |      :
Db        119 PNYMGLEFKKHHDYYITSTSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTT 178

Qy        182 SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
              |    | |     : : ||     ||      :   |    |       ||:|| :
Db        179 SRPSKEADNTVKMATQAPGSRGSLGDSDGKHETVNQEEKSGP-------GASGGSSGDPD 231

Qy        237 ------LLLLGVAGAGGA-------------MCWRRRRAKPSESRHPGPGSFGRGGSLGL 277
                    : |    |||                :  |:|  | ::          |  :| |
Db        232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLKLRKRHRKHTQQ---------RAAALSL 282

Qy        278 ----GGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
                   || |    || :: | ||     :  :||||||||||||||||||: |||||
Db        283 STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP 339

Qy        334 PNIYY 338
               ||||
Db        340 ANIYY 344
```

RESULT 12
US-08-436-044-4
; Sequence 4, Application US/08436044
; Patent No. 5624899
; GENERAL INFORMATION:
; APPLICANT: Bennett, Brian D.
; APPLICANT: Matthews, William
; TITLE OF INVENTION: HTK LIGAND
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,044
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/277722
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 902D3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881

```
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  333 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-436-044-4

  Query Match             25.3%;  Score 620.5;  DB 1;  Length 333;
  Best Local Similarity   40.5%;  Pred. No. 3.8e-44;
  Matches  133;  Conservative   52;  Mismatches  130;  Indels   13;  Gaps    5;

Qy         14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
              | |::|    :   : |||:||||:| :|    | ||||||||:||::||:       :
Db         14 GVLMVLCRTAISKSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 70

Qy         74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
                ||:||:|:|   |  ||        || | :|| |::|||||||:|||||| ||: :
Db         71 GQYEYYKVYMVDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK 130

Qy        134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
              |||||:||:|: |||:: :|||| || ||:|::|||  |  |    : |     :|
Db        131 DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN 190

Qy        191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
              | : :  |  :  ||  |   ::  :   :    :   || | |  : :: :      :
Db        191 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLL 250

Qy        251 WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
                |||  :    :|    |     :    |        :|| :: | ||    ||  ||||
Db        251 KYRRRHRKHSPQHTTTLSLSTLATPKRSGNN----NGSEPSDIIIPLR---TADSVFCPH 303

Qy        311 YEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
              ||||||||||||||: ||||| ||||
Db        304 YEKVSGDYGHPVYIVQEMPPQSPANIYY 331


RESULT 13
US-08-436-054-4
; Sequence 4, Application US/08436054
; Patent No. 5864020
;  GENERAL INFORMATION:
;    APPLICANT:  Bennett, Brian D.
;    APPLICANT:  Matthews, William
;    TITLE OF INVENTION:  HTK LIGAND
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
```

```
;       SOFTWARE:  patin (Genentech)
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/436,054
;       FILING DATE:  05-MAY-1995
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/277722
;       FILING DATE:  20-JUL-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Lee, Wendy M.
;       REGISTRATION NUMBER:  00,000
;       REFERENCE/DOCKET NUMBER:  902D1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415/225-1994
;       TELEFAX:  415/952-9881
;       TELEX:  910/371-7168
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  333 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
US-08-436-054-4

  Query Match             25.3%;  Score 620.5;  DB 2;  Length 333;
  Best Local Similarity   40.5%;  Pred. No. 3.8e-44;
  Matches  133;  Conservative   52;  Mismatches  130;  Indels   13;  Gaps    5;

Qy         14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
              | |::|    :   : |||:||||:| :|    | ||||||||:||::||:       :
Db         14 GVLMVLCRTAISKSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 70

Qy         74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
                ||:||:|:|   |  ||        || | :|| |::||||||:|||||| ||: :
Db         71 GQYEYYKVYMVDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK 130

Qy        134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
              |||||:||:|: |||:: :|||| || ||:|::|||  |  |    : |     :|
Db        131 DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN 190

Qy        191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
              | : :  |  :  ||  |   ::  :   :    :   || | |  : :: :      :
Db        191 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLL 250

Qy        251 WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
                ||| :    :|    |     :    |        :|| :: | ||    ||  ||||
Db        251 KYRRRHRKHSPQHTTTLSLSTLATPKRSGNN----NGSEPSDIIIPLR---TADSVFCPH 303

Qy        311 YEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
              |||||||||||||||: ||||| ||||
Db        304 YEKVSGDYGHPVYIVQEMPPQSPANIYY 331


RESULT 14
US-08-271-948-2
; Sequence 2, Application US/08271948
; Patent No. 6303769
;  GENERAL INFORMATION:
```

```
;    APPLICANT:  Cerretti, Douglas P.
;    APPLICANT:  Reddy, Pranhitha
;    TITLE OF INVENTION:  No. 6303769el Cytokine Designated Lerk-5
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  US
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Apple 7.1
;      SOFTWARE:  Microsoft Word, Version 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/271,948
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seese, Kathryn A.
;      REGISTRATION NUMBER:  32,172
;      REFERENCE/DOCKET NUMBER:  2823
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 587-0430
;      TELEFAX:  (206) 233-0644
;      TELEX:  756822
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  333 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-271-948-2

  Query Match             25.3%;  Score 620.5;  DB 4;  Length 333;
  Best Local Similarity   40.5%;  Pred. No. 3.8e-44;
  Matches  133;  Conservative   52;  Mismatches  130;  Indels   13;  Gaps    5;

Qy         14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
              | |::|    :   : |||:||||:| :|    | ||||||||:||::||:       :
Db         14 GVLMVLCRTAISKSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 70

Qy         74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
               ||:||:|:|   |  ||        || | :|| |::|||||||:|||||| ||: :
Db         71 GQYEYYKVYMVDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK 130

Qy        134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
              |||||:||:|: |||:: :|||| || ||:|::|||  |  |    : |     :|
Db        131 DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN 190

Qy        191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
              | : :  |  :  ||  |   ::  :   :    :   || | |  : :: :      :
Db        191 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLL 250

Qy        251 WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
```

```
                ||| :    :|    |     :    |        :|| :: | ||    ||  ||||
Db        251 KYRRRHRKHSPQHTTTLSLSTLATPKRSGNN----NGSEPSDIIIPLR---TADSVFCPH 303

Qy        311 YEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
              ||||||||||||||||: ||||| ||||
Db        304 YEKVSGDYGHPVYIVQEMPPQSPANIYY 331


RESULT 15
US-08-739-333-2
; Sequence 2, Application US/08739333
; Patent No. 6479459
;  GENERAL INFORMATION:
;    APPLICANT:  Cerretti, Douglas P.
;    APPLICANT:  Reddy, Pranhitha
;    TITLE OF INVENTION:  No. 6479459el Cytokine Designated Lerk-5
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  US
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Apple 7.1
;      SOFTWARE:  Microsoft Word, Version 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/739,333
;      FILING DATE:  29-OCT-1996
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/271,948
;      FILING DATE:  08-JUL-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seese, Kathryn A.
;      REGISTRATION NUMBER:  32,172
;      REFERENCE/DOCKET NUMBER:  2823
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 587-0430
;      TELEFAX:  (206) 233-0644
;      TELEX:  756822
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  333 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-739-333-2

  Query Match             25.3%;  Score 620.5;  DB 4;  Length 333;
  Best Local Similarity   40.5%;  Pred. No. 3.8e-44;
  Matches  133;  Conservative   52;  Mismatches  130;  Indels   13;  Gaps    5;

Qy         14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
```

```
                | |::|    :   : |||:||||:| :|    | ||||||||:||::||:       :
Db         14 GVLMVLCRTAISKSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 70

Qy         74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
             ||:||:|:|   |  ||        || | :|| |::||||||:|||||| ||: :
Db         71 GQYEYYKVYMVDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK 130

Qy        134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
             |||||:||:|: |||:: :|||| || ||:|::|||  |  |    : |     :|
Db        131 DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN 190

Qy        191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
             | : :  |  :  ||  |   ::  :   :    :   || | |  : :: :      :
Db        191 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLL 250

Qy        251 WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
              ||| :    :|    |     :    |        :|| :: | ||    ||  ||||
Db        251 KYRRRHRKHSPQHTTTLSLSTLATPKRSGNN----NGSEPSDIIIPLR---TADSVFCPH 303

Qy        311 YEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
             ||||||||||||||||: ||||| ||||
Db        304 YEKVSGDYGHPVYIVQEMPPQSPANIYY 331


Search completed: April 13, 2004, 09:29:17
Job time : 34.6226 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 13, 2004, 09:22:17 ; Search time 19.4591 Seconds
(without alignments)
2249.184 Million cell updates/sec

Title: US-10-021-121-2
Perfect score: 2450
Sequence: 1 MGPPHSGPGGVRVGALLLLG.....TTLLRQRASVEAEAGQHGPL 455

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	628.5	25.7	336	2	I49766	hepatoma transmemb
2	623	25.4	346	2	S46993	elk ligand - human
3	620.5	25.3	333	2	I84743	hepatoma transmemb
4	604.5	24.7	345	2	I48780	Stra1/Eplg2 protei
5	599.5	24.5	345	2	I58406	LERK-2 - rat
6	214.5	8.8	237	2	T19914	hypothetical prote
7	179	7.3	238	2	I38849	LERK-3 - human
8	176	7.2	209	2	A54984	ELF-1 protein prec
9	175.5	7.2	213	2	JE0322	ephrin-A2 - human
10	170.5	7.0	228	2	A57084	repulsive axon gui
11	169.5	6.9	201	2	I38850	LERK-4 - human
12	167.5	6.8	228	2	I58170	LERK-7 precursor -
13	166	6.8	205	2	A36377	B61 protein precur

14	159	6.5	680	2	S31216	collagen alpha 1(X
15	154.5	6.3	1049	1	CGBO7S	collagen alpha 1(I
16	153.5	6.3	1670	1	CGHU3B	collagen alpha 3(I
17	151.5	6.2	301	2	B31219	collagen 2 - Caeno
18	149	6.1	325	2	T32248	hypothetical prote
19	149	6.1	569	2	S42886	collagen - silkwor
20	148.5	6.1	316	2	T20497	hypothetical prote
21	148	6.0	921	2	S42617	collagen alpha 1(I
22	146.5	6.0	1315	2	A56101	collagen alpha 1(X
23	146.5	6.0	1492	2	A40333	collagen alpha 1'(
24	146.5	6.0	1774	2	B56101	collagen alpha 1(X
25	146	6.0	675	2	S20819	collagen alpha 3(I
26	145.5	5.9	305	2	T20906	hypothetical prote
27	145	5.9	674	2	S13301	collagen alpha 1(X
28	145	5.9	931	2	S13580	collagen alpha 1(I
29	144.5	5.9	438	2	S53787	collagen alpha cha
30	144	5.9	1027	2	S28774	collagen alpha cha
31	143	5.8	1747	2	A54121	collagen alpha-4 c
32	142.5	5.8	635	2	A57131	collagen alpha 2(V
33	142.5	5.8	743	1	S23779	collagen alpha 1(V
34	142.5	5.8	1496	1	CGHU2V	collagen alpha 2(V
35	142	5.8	614	2	T33149	hypothetical prote
36	142	5.8	744	2	S15435	collagen alpha 1(V
37	142	5.8	1029	1	S21369	collagen alpha 2(V
38	142	5.8	1763	2	S16366	collagen alpha 2(I
39	141.5	5.8	1466	1	CGHU7L	collagen alpha 1(I
40	141	5.8	319	2	T32250	hypothetical prote
41	141	5.8	744	1	A34246	collagen alpha 1(V
42	141	5.8	744	1	S23298	collagen alpha 1(V
43	140.5	5.7	305	2	T30165	hypothetical prote
44	140	5.7	304	2	T22482	hypothetical prote
45	140	5.7	680	1	CGHU1D	collagen alpha 1(X

ALIGNMENTS

RESULT 1
I49766
hepatoma transmembrane kinase ligand - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C;Accession: I49766
R;Bennett, B.D.; Zeigler, F.C.; Gu, Q.; Fendly, B.; Goddard, A.D.; Gillett, N.; Matthews, W.
Proc. Natl. Acad. Sci. U.S.A. 92, 1866-1870, 1995
A;Title: Molecular cloning of a ligand for the EPH-related receptor protein-tyrosine kinase Htk.
A;Reference number: I49766; MUID:95199254; PMID:7534404
A;Accession: I49766
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-336 <RES>
A;Cross-references: GB:L38847; NID:g769677; PIDN:AAC42052.1; PID:g769678
C;Genetics:
A;Gene: HTK

```
  Query Match             25.7%;  Score 628.5;  DB 2;  Length 336;
  Best Local Similarity   41.8%;  Pred. No. 2.8e-37;
  Matches  137;  Conservative   49;  Mismatches  129;  Indels   13;  Gaps    5;

Qy         14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
              | |::|    :   : |||:||||:| :|    | ||||||||:||::||:       :
Db         17 GLLMVLCRTAISRSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 73

Qy         74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
                ||:||:|:|   |  ||        || | ||| |::|||||||:|||||| ||: :
Db         74 GQYEYYKVYMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK 133

Qy        134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
              |||||:||:|: |||:: :|||| || ||:|::|||  |  | |    |     :|
Db        134 DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSARNHGPTRRPELEAGTN 193

Qy        191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
              | : :  |  :  ||  |   ::  :   |    :   || | |  : :: :      :
Db        194 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIIFIVIIITLVVLLL 253

Qy        251 WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
                ||| :    :|    |     :   ||        :|| :: | ||    ||  ||||
Db        254 KYRRRHRKHSPQHTTTLSLSTLATPKRGGNN----NGSEPSDVIIPLR---TADSVFCPH 306

Qy        311 YEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
              ||||||||||||||||: ||||| ||||
Db        307 YEKVSGDYGHPVYIVQEMPPQSPANIYY 334


RESULT 2
S46993
elk ligand - human
C;Species: Homo sapiens (man)
C;Date: 15-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 28-May-1999
C;Accession: S46993
R;Beckmann, M.P.; Cerretti, D.P.; Baum, P.; vanden Bos, T.; James, L.; Farrah,
T.; Kozlosky, C.; Hollingsworth, T.; Shilling, H.; Maraskovsky, E.; Fletcher,
F.A.; Lhotak, V.; Pawson, T.; Lyman, S.D.
EMBO J. 13, 3757-3762, 1994
A;Title: Molecular characterization of a family of ligands for eph-related
tyrosine kinase receptors.
A;Reference number: S46993; MUID:94349923; PMID:8070404
A;Accession: S46993
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-346 <BEC>
A;Cross-references: GB:U09304; NID:g538366; PIDN:AAA53093.1; PID:g538367

  Query Match             25.4%;  Score 623;  DB 2;  Length 346;
  Best Local Similarity   39.2%;  Pred. No. 7.1e-37;
  Matches  143;  Conservative   48;  Mismatches  116;  Indels   58;  Gaps    9;

Qy          8 PGGVRVGALLLLGVLGLVSGL------SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
              ||   :|  |:  |:  :  |      :|||| |:| | :| :  | |:||:|||:||::
Db          4 PGQRWLGKWLVAMVVWALCRLATPLAKNLEPVSWSSSLNPKFLSGKGLVIYPKIGDKLDII 63

Qy         62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
```

```
                |||||     |      ||:||||||    |    |      ||:|:||:||: ::|||||||:|
Db          64 CPRAEAGRP-----YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118

Qy         122 PNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
                ||   | ||: |||||| :||:|: |||||: :|||| || ||::::||| |       :
Db         119 PNYMGLEFKKHHDYYITSTSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTT 178

Qy         182 SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
                |     | |      : : ||      ||       :    |     |        ||:|| :
Db         179 SRPSKEADNTVKMATQAPGSRGSLGDSDGKHETVNQEEKSGP-------GASGGSSGDPD 231

Qy         237 ------LLLLGVAGAGGA-------------MCWRRRRAKPSESRHPGPGSFGRGGSLGL 277
                     : |     |||                 :  |:|  | ::           |  :| |
Db         232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLKLRKRHRKHTQQ---------RAAALSL 282

Qy         278 ----GGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
                       || |     || :: | ||      :  :||||||||||||||||||: |||||
Db         283 STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP 339

Qy         334 PNIYY 338
                ||||
Db         340 ANIYY 344
```

RESULT 3
I84743
hepatoma transmembrane kinase ligand - human
C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 05-Nov-1999
C;Accession: I84743
R;Bennett, B.D.; Zeigler, F.C.; Gu, Q.; Fendly, B.; Goddard, A.D.; Gillett, N.; Matthews, W.
Proc. Natl. Acad. Sci. U.S.A. 92, 1866-1870, 1995
A;Title: Molecular cloning of a ligand for the EPH-related receptor protein-tyrosine kinase Htk.
A;Reference number: I49766; MUID:95199254; PMID:7534404
A;Accession: I84743
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-333 <RES>
A;Cross-references: GB:L38734; NID:g769675; PIDN:AAC41752.1; PID:g769676
C;Genetics:
A;Gene: GDB:EPLG5; LERK5
A;Cross-references: GDB:438338; OMIM:600527
A;Map position: 13q33-13q33

  Query Match   25.3%; Score 620.5; DB 2; Length 333;
  Best Local Similarity   40.5%; Pred. No. 1e-36;
  Matches 133; Conservative   52; Mismatches 130; Indels   13; Gaps   5;

```
Qy          14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
               | |::|    :   : |||:||||:| :|    | ||||||||:||::||:       :
Db          14 GVLMVLCRTAISKSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 70

Qy          74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
                 ||:||:|:|   |  ||        || | :|| |::||||||:|||||| ||: :
Db          71 GQYEYYKVYMVDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK 130
```

```
Qy        134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
              |||||:||:|: |||:: :|||| || ||:|::||| | | : | :|
Db        131 DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN 190

Qy        191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
              | : : | : || | :: : : : || | | : :: :      :
Db        191 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLL 250

Qy        251 WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
                ||| :    :|    |     :    |        :|| :: | ||    ||  ||||
Db        251 KYRRRHRKHSPQHTTTLSLSTLATPKRSGNN----NGSEPSDIIIPLR---TADSVFCPH 303

Qy        311 YEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
              ||||||||||||||||: ||||| ||||
Db        304 YEKVSGDYGHPVYIVQEMPPQSPANIYY 331
```

RESULT 4
I48780
Stra1/Eplg2 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C;Accession: I48780; A55507; A55062; S52670
R;Bouillet, P.; Oulad-Abdelghani, M.; Vicaire, S.; Garnier, J.M.; Schuhbaur, B.; Dolle, P.; Chambon, P.
Dev. Biol. 170, 420-433, 1995
A;Title: Efficient cloning of cDNAs of retinoic acid-responsive genes in P19 embryonal carcinoma cells and characterization of a novel mouse gene, Stra1 (mouse LERK-2/Eplg2).
A;Reference number: I48780; MUID:95377533; PMID:7649373
A;Accession: I48780
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-345 <RES>
A;Cross-references: EMBL:Z48781; NID:g747858; PIDN:CAA88695.1; PID:g747859
R;Fletcher, F.A.; Renshaw, B.; Hollingsworth, T.; Baum, P.; Lyman, S.D.; Jenkins, N.A.; Gilbert, D.J.; Copeland, N.G.; Davison, B.L.
Genomics 24, 127-132, 1994
A;Title: Genomic organization and chromosomal localization of mouse Eplg2, a gene encoding a binding protein for the receptor tyrosine kinase Elk.
A;Reference number: A55507; MUID:95203867; PMID:7896266
A;Accession: A55507
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-345 <FLE>
A;Cross-references: GB:U07598
R;Shao, H.; Lou, L.; Pandey, A.; Pasquale, E.B.; Dixit, V.M.
J. Biol. Chem. 269, 26606-26609, 1994
A;Title: cDNA cloning and characterization of a ligand for the Cek5 receptor protein-tyrosine kinase.
A;Reference number: A55062; MUID:95014510; PMID:7929389
A;Accession: A55062
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-89,'T',91-345 <SHA>
A;Cross-references: GB:U12983; NID:g575928; PIDN:AAA53231.1; PID:g575929

C;Genetics:
A;Gene: EPLG2

Query Match 24.7%; Score 604.5; DB 2; Length 345;
Best Local Similarity 37.9%; Pred. No. 1.5e-35;
Matches 136; Conservative 51; Mismatches 107; Indels 65; Gaps 10;

```
Qy         15 ALLLLGVLGLVSGL--SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHS 72
              |:::| :  | : |  :|||| |:| | :| :  | |:||:|||:||::|||| |
Db         15 AMVVLTLCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDIICPRAEAGRP-- 72

Qy         73 SPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSH 132
                ||:||||||  |  |    ||:|:||::| ::|||||||||:|||  | ||: :
Db         73 ---YEYYKLYLVRPEQAAACSTVLDPNVLVTCNKPHQEIRFTIKFQEFSPNYMGLEFKKY 129

Qy        133 HDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGA 192
              ||||| :||:|: ||||: :|||| || ||::::||| |     | :  :  | :
Db        130 HDYYITSTSNGSLEGLENREGGVCRTRTMKIVMKVGQDP-NAVTPEQLTTSRPSKESDNT 188

Qy        193 AHSLEPGKENLPGDPTSNATSRGAEGP---------LPPPSMPAVAGAAGG-------LA 236
               :           : |  ||::|              | |   |   |
Db        189 VKT-----------ATQAPGRGSQGDSDGKHETVNQEEKSGPGAGGGGSGDSDSFFNSK 236

Qy        237 LLLLGVAGAGGA-------------MCWRRRRAKPSESRHPGPGSFGRGGSLGL----GG 279
              : |    |||               :  |:|  | ::          |  :| |
Db        237 VALFAAVGAGCVIFLLIIIFLTVLLLKLRKRHRKHTQQ---------RAAALSLSTLASP 287

Qy        280 GGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
               || |    || :: | ||     :  :|||||||||||||||||: ||||| ||||
Db        288 KGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSPANIYY 343
```

RESULT 5
I58406
LERK-2 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C;Accession: I58406
R;Fletcher, F.A.; Carpenter, M.; Shilling, H.; Baum, P.; Ziegler, S.; Gimpel, S.; Hollingsworth, T.; VandenBos, T.; Davison, B.L.; Lyman, S.D.; Beckmann, M.P.
Oncogene 9, 3241-3248, 1994
A;Title: LERK-2, a ligand for the receptor tyrosine kinase ELK, is evolutionarily conserved and expressed in a developmentally regulated pattern.
A;Reference number: I58406; MUID:95022634; PMID:7936648
A;Accession: I58406
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-345 <RES>
A;Cross-references: EMBL:U07560; NID:g563118; PIDN:AAA53092.1; PID:g563119
C;Genetics:
A;Gene: Eplg2

Query Match 24.5%; Score 599.5; DB 2; Length 345;
Best Local Similarity 37.6%; Pred. No. 3.3e-35;
Matches 135; Conservative 52; Mismatches 107; Indels 65; Gaps 10;

```
Qy         15 ALLLLGVLGLVSGL--SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHS 72
```

```
            |:::| :  | : |  :|||| |:| | :| :  | |:||:|||:||::|||| |
Db          15 AMVVLTLCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDIICPRAEAGRP-- 72

Qy          73 SPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSH 132
               ||:|||||  |  |    ||:|:||::|  ::|||||||:|||  | ||: :
Db          73 ---YEYYKLYLVRPEQAAACSTVLDPNVLVTCNKPQQEIRFTIKFQEFSPNYMGLEFKKY 129

Qy         133 HDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGA 192
               ||||| :||:|: |||||: :|||| || ||::::||| |    | :  :  | :
Db         130 HDYYITSTSNGSLEGLENREGGVCRTRTMKIVMKVGQDP-NAVTPEQLTTSRPSKESDNT 188

Qy         193 AHSLEPGKENLPGDPTSNATSRGAEGP---------LPPPSMPAVAGAAGG-------LA 236
                 :            : |  ||::|             | |   |:  |
Db         189 VKT------------ATQAPGRGSQGDSDGKHETVNQQEKSGPGAGGSGSGDTDSFFNSK 236

Qy         237 LLLLGVAGAGGA-------------MCWRRRRAKPSESRHPGPGSFGRGGSLGL----GG 279
               : |    |||               :  |:|  | ::          |  :| |
Db         237 VALFAAVGAGCVIFLLIIIFLTVLLLKLRKRHRKHTQQ---------RAAALSLSTLASP 287

Qy         280 GGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
                | |    || :: | ||     :  :|||||||||||||||||||: ||||| ||||
Db         288 KGDSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSPANIYY 343
```

RESULT 6
T19914
hypothetical protein C43F9.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T19914
R;Mortimore, B.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19195
A;Accession: T19914
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-237 <WIL>
A;Cross-references: EMBL:Z82262; PIDN:CAB54195.1; GSPDB:GN00022; CESP:C43F9.8
A;Experimental source: clone C43F9
C;Genetics:
A;Gene: CESP:C43F9.8
A;Map position: 4
A;Introns: 32/2; 96/3; 214/1

Query Match 8.8%; Score 214.5; DB 2; Length 237;
Best Local Similarity 25.7%; Pred. No. 3.9e-08;
Matches 53; Conservative 41; Mismatches 83; Indels 29; Gaps 6;

```
Qy          11 VRVGALLLLGVLGLVS-GLSLEPVYWNSANKRFQAEG-GYVLYPQIGDRLDLLCPRARPP 68
               :::   :|| :   :     :  : | |:|  |      :|:   ||||: : ||::
Db           1 MQIATFILLSLFPFIGWARKIPDINWISSNPIFDVSNTDHVISVHIGDRVSIRCPKSDET 60

Qy          69 GPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHE 128
               |      ||:  :|:|   :   |     | |:  ||   ::    | |: ::|   | |
Db          61 G-----KYEYSYIYMVSDEEYDHCFL-SKPRLVGACDNQTINASINIVFRSFTPTPGGFE 114

Qy         129 FRSHHDYYIIA------------------TSDGTREGLESLQGGVCLTRGMKVLLRVGQ 169
```

```
              |:   :|::|:                    |||||  ||::  : |:|  : ||:   |||
Db        115 FQPGKNYFLISKSEVDALIIYETANQIFPGTSDGTLEGIDRKKDGLCTAKQMKIKFEVGQ 174

Qy        170 SPRGGAVPRKPVSEMPMERDRGAAHS 195
                ||   |:   :   :::|| | ||
Db        175 DRRGIENPK--FAARTLKKDRDAEHS 198


RESULT 7
I38849
LERK-3 - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 29-Sep-1999
C;Accession: I38849
R;Kozlosky, C.J.; Maraskovsky, E.; McGrew, J.T.; VandenBos, T.; Teepe, M.;
Lyman, S.D.; Srinivasan, S.; Fletcher, F.A.; Gayle, R.B.
Oncogene 10, 299-306, 1995
A;Title: Ligands for the receptor tyrosine kinases hek and elk: isolation of
cDNAs encoding a family of proteins.
A;Reference number: I38849; MUID:95140419; PMID:7838529
A;Accession: I38849
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-238 <RES>
A;Cross-references: EMBL:U14187; NID:g642832; PIDN:AAC50078.1; PID:g642833
C;Genetics:
A;Gene: GDB:EPLG3
A;Cross-references: GDB:438336; OMIM:601381
A;Map position: 1q21-1q22
C;Superfamily: axon guidance signal protein

  Query Match             7.3%;  Score 179;  DB 2;  Length 238;
  Best Local Similarity   28.4%;  Pred. No. 1.3e-05;
  Matches   65;  Conservative   24;  Mismatches   80;  Indels   60;  Gaps   12;

Qy          7 GPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCP--R 64
              |||           | ||     :   |||||:|:  : | || :   : | ||: ||
Db         24 GPG----------GALG-----NRHAVYWNSSNQHLRRE-GYTVQVNVNDYLDIYCPHYN 67

Qy         65 ARPPGPHSSP----NYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKF 117
              :   || : |      | | ||:|     | | |         |:||      ::|: ||
Db         68 SSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFK-RWECNRPHAPHSPIKFSEKF 126

Qy        118 QEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVP 177
              | ||    |:|| : |:|| |:|                ||   ||| :    :   |
Db        127 QRYSAFSLGYEFHAGHEYYYISTPTHNLH-------WKCLR--MKVFVCCASTSHSG--- 174

Qy        178 RKPVSEMP---------------MERDRGAAHSLE-------PGKENLP 204
              |||  :|               | :      ||       | :|:||
Db        175 EKPVPTLPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLP 223


RESULT 8
A54984
ELF-1 protein precursor - mouse
N;Alternate names: Cek7 ligand
C;Species: Mus musculus (house mouse)
```

C;Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 29-Sep-1999
C;Accession: A54984; A55873
R;Cheng, H.J.; Flanagan, J.G.
Cell 79, 157-168, 1994
A;Title: Identification and cloning of ELF-1, a developmentally expressed ligand for the Mek4 and Sek receptor tyrosine kinases.
A;Reference number: A54984; MUID:95007776; PMID:7522971
A;Accession: A54984
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-209 <CHE>
A;Cross-references: GB:U14941; NID:g558836; PIDN:AAA53636.1; PID:g558837
R;Shao, H.; Lou, L.; Pandey, A.; Verderame, M.F.; Siever, D.A.; Dixit, V.M.
J. Biol. Chem. 270, 3467-3470, 1995
A;Title: cDNA cloning and characterization of a Cek7 receptor protein-tyrosine kinase ligand that is identical to the ligand (ELF-1) for the Mek-4 and Sek receptor protein-tyrosine kinases.
A;Reference number: A55873; MUID:95181289; PMID:7876076
A;Accession: A55873
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-209 <SHA>
A;Cross-references: GB:U14752; NID:g681886; PIDN:AAA68520.1; PID:g681887
C;Superfamily: axon guidance signal protein
C;Keywords: lipoprotein; membrane protein

Query Match 7.2%; Score 176; DB 2; Length 209;
Best Local Similarity 29.3%; Pred. No. 1.8e-05;
Matches 58; Conservative 19; Mismatches 69; Indels 52; Gaps 7;

```
Qy         33 VYWNSANKRFQAE-----GGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGA 87
              |||| :| |||       ||| :   | | ||: ||    | |  :   | | ||:| |
Db         35 VYWNRSNPRFQVSAVGDGGGYTVEVSINDYLDIYCPHYGAPLP-PAERMERYILYMVNGE 93

Qy         88 QGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGT 144
                 |:          |:||      |:|: ||| ::|   | |||  |:|| |: :
Db         94 GHASCDHRQRGFKRWECNRPAAPGGPLKFSEKFQLFTPFSLGFEFRPGHEYYYISATP-- 151

Qy        145 REGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLP 204
                :|    ||   :|| :|                                  |  | |
Db        152 ----PNLVDRPCLR--LKVYVR-------------------------------PTNETLY 174

Qy        205 GDP----TSNATSRGAEG 218
                |    |||::  |  |
Db        175 EAPEPIFTSNSSCSGLGG 192
```

RESULT 9
JE0322
ephrin-A2 - human
C;Species: Homo sapiens (man)
C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jul-2000
C;Accession: JE0322
R;Aasheim, H.; Pedeutour, F.; Grosgeorge, J.; Logtenberg, T.
Biochem. Biophys. Res. Commun. 252, 378-382, 1998
A;Title: Cloning, chromosal mapping, and tissue expression of the gene encoding the human Eph-family kinase ligand ephrin-A2.

A;Reference number: JE0322; MUID:99045414; PMID:9826538
A;Accession: JE0322
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-213 <AAS>
A;Cross-references: GB:AJ007292; NID:g3688367; PIDN:CAA07435.1; PID:g3688368
C;Superfamily: axon guidance signal protein

Query Match 7.2%; Score 175.5; DB 2; Length 213;
Best Local Similarity 36.8%; Pred. No. 2e-05;
Matches 43; Conservative 14; Mismatches 51; Indels 9; Gaps 3;

```
Qy         33 VYWNSANKRFQA-----EGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGA 87
              |||| :| || |      ||| :   | | ||: ||    | |  :   | | ||:| |
Db         39 VYWNRSNPRFHAGAGDDGGGYTVEVSINDYLDIYCPHYGAPLP-PAERMEHYVLYMVNGE 97

Qy         88 QGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHHDYYIIATS 141
                  |:          |:||      |:|: ||| ::|   | |||  |:|| |: :
Db         98 GHASCDHRQRGFKRWECNRPAAPGGPLKFSEKFQLFTPFSLGFEFRPGHEYYYISAT 154
```

RESULT 10
A57084
repulsive axon guidance signal protein RAGS precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 20-Jun-2000
C;Accession: A57084
R;Drescher, U.; Kremoser, C.; Handweker, C.; Loeschinger, J.; Noda, M.; Bonhoeffer, F.
Cell 82, 359-370, 1995
A;Title: In vitro guidance of retinal ganglion cell axons by RAGS, a 25 kDa tectal protein related to ligands for Eph receptor tyrosine kinases.
A;Reference number: A57084; MUID:95360980; PMID:7634326
A;Accession: A57084
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-228 <DRE>
A;Cross-references: GB:X90377; NID:g1061113; PIDN:CAA62027.1; PID:g984118
C;Superfamily: axon guidance signal protein
C;Keywords: glycoprotein; membrane protein; phosphatidylinositol linkage
F;1-20/Domain: signal sequence #status predicted <SIG>

Query Match 7.0%; Score 170.5; DB 2; Length 228;
Best Local Similarity 28.9%; Pred. No. 4.8e-05;
Matches 73; Conservative 30; Mismatches 91; Indels 59; Gaps 13;

```
Qy         16 LLLLGVLGL-VSGLSLEP----------VYWNSANKRFQAEGGYVLYPQIGDRLDLLCPR 64
              :||| |  | |     ||          ||||| | ||| :| | :   | | ||: ||
Db          6 MLLLAVAALWVCVRGQEPGRKAVADRYAVYWNSTNPRFQ-QGDYHIDVCINDYLDVFCPH 64

Qy         65 ARPPGPHSSPNYEFYKLYLVG----------GAQGRRCEAPPAPNLLLTCDRPDLDLR 112
                   |      | | ||:|             | :   |  | :||           |:
Db         65 YEDSVPEDKT--ERYVLYMVNFDGYSSCDHISKGFKRWECNRPHSPN---------GPLK 113

Qy        113 FTIKFQEYSPNLWGHEFRSHHDYYIIATS---DGTREGLESLQGGVCLTRGMKVLLRVGQ 169
              |: ||| ::|   | |||   :|: |:::   :| |          ||   :|| :|
Db        114 FSEKFQLFTPFSLGFEFRPGREYFYISSAIPDNGRRS---------CLK--LKVFVR--- 159
```

```
Qy        170 SPRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMP--A 227
                |    :    | :   : :    :||||  : :     |   ||| |     | :|
Db        160 -PANSCMKTIGVHDRVFDVNDKVENSLEPADDTV---RESAEPSRG-ENAAQTPRIPIRL 214

Qy        228 VAGAAGGLALLLL 240
              :|     ||:||:
Db        215 LATLLFLLAMLLI 227
```

RESULT 11
I38850
LERK-4 - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 29-Sep-1999
C;Accession: I38850
R;Kozlosky, C.J.; Maraskovsky, E.; McGrew, J.T.; VandenBos, T.; Teepe, M.; Lyman, S.D.; Srinivasan, S.; Fletcher, F.A.; Gayle, R.B.
Oncogene 10, 299-306, 1995
A;Title: Ligands for the receptor tyrosine kinases hek and elk: isolation of cDNAs encoding a family of proteins.
A;Reference number: I38849; MUID:95140419; PMID:7838529
A;Accession: I38850
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-201 <RES>
A;Cross-references: EMBL:U14188; NID:g642834; PIDN:AAC50079.1; PID:g642835
C;Genetics:
A;Gene: GDB:EPLG4
A;Cross-references: GDB:438337; OMIM:601380
A;Map position: 1q21-1q22
C;Superfamily: axon guidance signal protein

  Query Match   6.9%; Score 169.5; DB 2; Length 201;
  Best Local Similarity   29.9%; Pred. No. 5e-05;
  Matches   66; Conservative   18; Mismatches   82; Indels   55; Gaps   10;

```
Qy         24 LVSGLSL-EPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLY 82
              |  | ||   |||||:| |    |  |:   : | ||::||    |||   |  | : ||
Db         20 LRGGSSLRHVVYWNSSNPRL-LRGDAVVELGLNDYLDIVCPHYEGPGPPEGP--ETFALY 76

Qy         83 LVGGAQGRRCEAP-PAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATS 141
              :|       |:|  |       |  |   ::|: | | ::|   | ||     || |:
Db         77 MVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSLGFEFLPGETYYYISVP 136

Qy        142 DGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLEPGKE 201
               | |       | ||                    |  ||    ||   :|| :
Db        137 --TPE-----SSGQCL--------------------RLQVSVCCKERKSESAHPV----- 164

Qy        202 NLPGDPTSNATS--RGAEGPLPPPSMPAVAGAAGGLALLLL 240
               | |  : ||  || : | |             | ||||
Db        165 ---GSPGESGTSGWRGGDTPSP------------LCLLLL 189
```

RESULT 12
I58170
LERK-7 precursor - human

N;Alternate names: AL-1
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999
C;Accession: I58170; G01812
R;Winslow, J.W.; Moran, P.; Valverde, J.; Shih, A.; Yuan, J.Q.; Wong, S.C.; Tsai, S.P.; Goddard, A.; Henzel, W.J.; Hefti, F.
Neuron 14, 973-981, 1995
A;Title: Cloning of AL-1, a ligand for an Eph-related tyrosine kinase receptor involved in axon bundle formation.
A;Reference number: I58170; MUID:95267434; PMID:7748564
A;Accession: I58170
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-228 <RES>
A;Cross-references: GB:S77167; NID:g914184; PID:g914185
R;Kozlosky, C.J.; VandenBos, T.; Park, L.S.; Cerretti, D.P.; Carpenter, M.K.
submitted to the EMBL Data Library, May 1995
A;Reference number: G08477
A;Accession: G01812
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-228 <KOZ>
A;Cross-references: EMBL:U26403; NID:g1019430; PIDN:AAB60377.1; PID:g1019431
C;Genetics:
A;Gene: GDB:EPLG7; AF1; LERK7
A;Cross-references: GDB:568757; OMIM:601535
A;Map position: 13q33-13q33
C;Superfamily: axon guidance signal protein

  Query Match 6.8%; Score 167.5; DB 2; Length 228;
  Best Local Similarity 28.8%; Pred. No. 7.9e-05;
  Matches 65; Conservative 29; Mismatches 81; Indels 51; Gaps 11;

```
Qy         33 VYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVG------- 85
              |||||:| |||  | | :   | | ||: ||      |      | | ||:|
Db         34 VYWNSSNPRFQ-RGDYHIDVCINDYLDVFCPHYEDSVPEDKT--ERYVLYMVNFDGYSAC 90

Qy         86 -----GAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIAT 140
                    | :   |  | :||           |:|: ||| ::|   | |||   :|: |::
Db         91 DHTSKGFKRWECNRPHSPN---------GPLKFSEKFQLFTPFSLGFEFRPGREYFYISS 141

Qy        141 S---DGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLE 197
              :   :| |          ||   :|| :|    |    :    | :   : :    :|||
Db        142 AIPDNGRRS---------CLK--LKVFVR----PTNSCMKTIGVHDRVFDVNDKVENSLE 186

Qy        198 PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVA 243
              |  : :     |   ||| |     | :|:       ||:||  :|
Db        187 PADDTV---HESAEPSRG-ENAAQTPRIPSRL-----LAILLFLLA 223
```

RESULT 13
A36377
B61 protein precursor - human
C;Species: Homo sapiens (man)
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 29-Sep-1999
C;Accession: A36377
R;Holzman, L.B.; Marks, R.M.; Dixit, V.M.

Mol. Cell. Biol. 10, 5830-5838, 1990
A;Title: A novel immediate-early response gene of endothelium is induced by cytokines and encodes a secreted protein.
A;Reference number: A36377; MUID:91042512; PMID:2233719
A;Accession: A36377
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-205 <HOL>
A;Cross-references: GB:M57730; GB:M37476; NID:g179320; PIDN:AAA58388.1; PID:g179321
C;Superfamily: axon guidance signal protein

Query Match 6.8%; Score 166; DB 2; Length 205;
Best Local Similarity 27.5%; Pred. No. 9e-05;
Matches 46; Conservative 31; Mismatches 74; Indels 16; Gaps 5;

```
Qy         18 LLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPN-- 75
              |||:   ::      |:|||:| :|: |  | :: |: | :|::||       ||  :
Db          8 LLGLCCSLAAADRHTVFWNSSNPKFRNE-DYTIHVQLNDYVDIICPHYE---DHSVADAA 63

Qy         76 YEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSH 132
               | | ||||   : : |:      :   |:||       : : ||| ::|   | ||:
Db         64 MEQYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKEFKEG 123

Qy        133 HDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRK 179
              | || |:      |         ||   : |  ::  ||:    |::
Db        124 HSYYYISKPIHQHEDR-------CLRLKVTVSGKITHSPQAHVNPQE 163
```

RESULT 14
S31216
collagen alpha 1(X) chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C;Accession: S31216; S28807; S22215; S30127; I48299; S26397; S31830
R;Kong, R.Y.C.; Kwan, K.M.; Lau, E.T.; Thomas, J.T.; Boot-Handford, R.P.; Grant, M.E.; Cheah, K.S.E.
Eur. J. Biochem. 213, 99-111, 1993
A;Title: Intron-exon structure, alternative use of promoter and expression of the mouse collagen X gene, Col10a-1.
A;Reference number: S31216; MUID:93238750; PMID:8477738
A;Accession: S31216
A;Molecule type: DNA
A;Residues: 1-680 <KON>
A;Cross-references: EMBL:Z21610; NID:g49793; PIDN:CAA79736.1; PID:g49794
R;Elima, K.; Eerola, I.; Rosati, R.; Metsaeranta, M.; Garofalo, S.; Peraelae, M.; de Crombrugghe, B.; Vuorio, E.
Biochem. J. 289, 247-253, 1993
A;Title: The mouse collagen X gene: complete nucleotide sequence, exon structure and expression pattern.
A;Reference number: S28807; MUID:93143676; PMID:8424763
A;Accession: S28807
A;Molecule type: DNA
A;Residues: 1-285,'A',287-680 <ELI>
A;Cross-references: EMBL:X67348; NID:g50480; PIDN:CAA47763.1; PID:g50481
R;Elima, K.; Metsaeranta, M.; Kallio, J.; Peraelae, M.; Eerola, I.; Garofalo, S.; de Crombrugghe, B.; Vuorio, E.

Biochim. Biophys. Acta 1130, 78-80, 1992
A;Title: Specific hybridization probes for mouse alpha-2(IX) and alpha-1(X) collagen mRNAs.
A;Reference number: S22215; MUID:92182017; PMID:1543751
A;Accession: S22215
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 385-450,'K',452-627 <ELA>
A;Cross-references: EMBL:X63013; NID:g49795; PIDN:CAA44741.1; PID:g49796
R;Apte, S.S.; Olsen, B.R.
Matrix 13, 165-179, 1993
A;Title: Characterization of the mouse type X collagen gene.
A;Reference number: S30127; MUID:93261348; PMID:8492743
A;Accession: S30127
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-12,'F',14-26,'S',28-247,'L',249-285,'A',287-305,'F',307-416,'S',418-499,'L',501-566,'C',568,'H',570,'IY',573-634,'T',636-680 <APT>
R;Apte, S.S.; Seldin, M.F.; Hayashi, M.; Olsen, B.R.
Eur. J. Biochem. 206, 217-224, 1992
A;Title: Cloning of the human and mouse type X collagen genes and mapping of the mouse type X collagen gene to chromosome 10.
A;Reference number: I48299; MUID:92267014; PMID:1587271
A;Accession: I48299
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 52-247,'L',249-285,'A',287-305,'F',307-416,'S',418-499,'L',501-566,'C',568,'H',570,'IY',573-634,'T',636-680 <RES>
A;Cross-references: EMBL:X65121; NID:g50482; PIDN:CAA46237.1; PID:g667031
R;Summers, T.A.; Irwin, M.H.; Mayne, R.; Balian, G.
J. Biol. Chem. 263, 581-587, 1988
A;Title: Monoclonal antibodies to type X collagen. Biosynthetic studies using an antibody to the amino-terminal domain.
A;Reference number: S26397; MUID:88087150; PMID:2826450
A;Accession: S26397
A;Molecule type: protein
A;Residues: 'SDGYFSQ',24-26,'KQ' <SUM>
C;Genetics:
A;Gene: Col10a-1
A;Map position: 10
A;Introns: 51/3
C;Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology
C;Keywords: coiled coil; extracellular matrix; glycoprotein; homotrimer
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-680/Product: collagen alpha 1(X) chain #status predicted <MAT>
F;553-679/Domain: complement C1q carboxyl-terminal homology <C1Q>

Query Match 6.5%; Score 159; DB 2; Length 680;
Best Local Similarity 25.5%; Pred. No. 0.0011;
Matches 97; Conservative 30; Mismatches 108; Indels 146; Gaps 24;

```
Qy          1 MGPPHSGPGGV-RVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLD 59
              :|||  || || | |     |  |:             :: |  | |
Db        211 IGPP--GPSGVGRRGENGFPGQPGI----------KGDRGFPGEMG---------- 244

Qy         60 LLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQE 119
```

```
                 : ||||   |           | |||  |    |  : :  :| :
Db        245 ----PSGPPGPQGPP----------GKQGR--EGIGKPGAIGSPGQPGI---------- 277

Qy        120 YSPNLWGHEFRSHHDYYIIATSDGT----REGLESLQGGVCLTRGMKVLLRVGQSPRGGA 175
                |   ||          ||   |     ::||  |:|     ||           | |
Db        278 --PGEKGHPGSPG-----IAGPPGAPGFGKQGLPGLRG----QRG----------PAG-- 314

Qy        176 VPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGL 235
              :|  | :    : :|| |    ||:  ||| |     : | :||   |    : || | :
Db        315 LPGAPGA----KGERGPAG--HPGEPGLPGSP----GNMGPQGPKGIPGNHGIPGAKGEI 364

Qy        236 ALLLLGVAGAGGAMCWRRRRAKP---SESRHPG----------PGSFGRGGSLGLGGGGG 282
                |:| ||  ||   |  |  |    :: :||          ||  |: |  |:||  |
Db        365 G--LVGPAGPPGA---RGARGPPGLDGKTGYPGEPGLNGPKGNPGLPGQKGDPGVGGTPG 419

Qy        283 M-------------------GPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVY 323
              :                   |||  |||  |      |   ||  | :    || |:|
Db        420 LRGPVGPVGAKGVPGHNGEAGPR-GEPGIPGTR----GPTGPPGVPGFPGSKGDPGNP-- 472

Qy        324 IVQDGP----------PQSPP 334
                ||          |  ||
Db        473 -GAPGPAGIATKGLNGPTGPP 492
```

RESULT 15
CGBO7S
collagen alpha 1(III) chain - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 07-May-1999
C;Accession: A02862; A38001; A38002; A38003; A38004; A38005; S71946
R;Fietzek, P.P.; Allmann, H.; Rauterberg, J.; Henkel, W.; Wachter, E.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 809-820, 1979
A;Title: The covalent structure of calf skin type III collagen. I. The amino acid sequence of the amino terminal region of the alpha1(III) chain (position 1-222).
A;Reference number: A02862; MUID:80026026; PMID:488906
A;Accession: A02862
A;Molecule type: protein
A;Residues: 1-242 <FIE>
R;Dewes, H.; Fietzek, P.P.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 821-832, 1979
A;Title: The covalent structure of calf skin type III collagen. II. The amino acid sequence of the cyanogen bromide peptide alpha1(III)CB1,8,10,2 (positions 223-402).
A;Reference number: A38001; MUID:80026027; PMID:488907
A;Accession: A38001
A;Molecule type: protein
A;Residues: 243-422 <DEW1>
R;Bentz, H.; Fietzek, P.P.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 833-840, 1979
A;Title: The covalent structure of calf skin type III collagen. III. The amino acid sequence of the cyanogen bromide peptide alpha1(III)CB4 (positions 403-551).
A;Reference number: A38002; MUID:80026028; PMID:488908
A;Accession: A38002
A;Molecule type: protein
A;Residues: 423-571 <BEN>

R;Lang, H.; Glanville, R.W.; Fietzek, P.P.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 841-850, 1979
A;Title: The covalent structure of calf skin type III collagen. IV. The amino acid sequence of the cyanogen bromide peptide alpha1(III)CB5 (positions 552-788).
A;Reference number: A38003; MUID:80026029; PMID:488909
A;Accession: A38003
A;Molecule type: protein
A;Residues: 572-808 <LAN>
R;Dewes, H.; Fietzek, P.P.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 851-860, 1979
A;Title: The covalent structure of calf skin type III collagen. V. The amino acid sequence of the cyanogen bromide peptide alpha1(III)CB9A (position 789 to 927).
A;Reference number: A38004; MUID:80026030; PMID:488910
A;Accession: A38004
A;Molecule type: protein
A;Residues: 809-947 <DEW2>
R;Allmann, H.; Fietzek, P.P.; Glanville, R.W.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 861-868, 1979
A;Title: The covalent structure of calf skin type III collagen. VI. The amino acid sequence of the carboxyterminal cyanogen bromide peptide alpha1(III)CB9B (position 928-1028).
A;Reference number: A38005; MUID:80026031; PMID:488911
A;Accession: A38005
A;Molecule type: protein
A;Residues: 948-1049 <ALL>
A;Experimental source: skin
R;Henkel, W.
Biochem. J. 318, 497-503, 1996
A;Title: Cross-link analysis of the C-telopeptide domain from type III collagen.
A;Reference number: S71946; MUID:96404897; PMID:8809038
A;Accession: S71946
A;Molecule type: protein
A;Residues: 87-106;1017-1029;1037-1049 <HEN>
C;Comment: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains.
C;Comment: The type III collagen molecule is a trimer of identical chains, linked to each other by interchain disulfide bonds. Trimers are also cross-linked by allysines forming desmosine.
C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology; von Willebrand factor type C repeat homology
C;Keywords: coiled coil; extracellular matrix; glycoprotein; hydroxylysine; hydroxyproline; skin; trimer; triple helix
F;1-1049/Product: collagen alpha 1(III) chain #status experimental <CAB>
F;1-14/Region: amino-terminal nonhelical telopeptide
F;15-1040/Region: helical
F;587-589/Region: cell attachment (R-G-D) motif
F;752-754/Region: cell attachment (R-G-D) motif
F;875-877/Region: cell attachment (R-G-D) motif
F;878-880/Region: cell attachment (R-G-D) motif
F;935-937/Region: cell attachment (R-G-D) motif
F;1041-1049/Region: carboxyl-terminal nonhelical telopeptide
F;95,107,119,938,950/Modified site: 5-hydroxylysine (Lys) #status experimental
F;107,950/Modified site: allysine (Lys) #status predicted
F;107/Binding site: carbohydrate (Lys) (covalent) #status experimental
F;1040,1041/Disulfide bonds: interchain #status predicted

Query Match 6.3%; Score 154.5; DB 1; Length 1049;
Best Local Similarity 26.5%; Pred. No. 0.0036;
Matches 60; Conservative 9; Mismatches 74; Indels 83; Gaps 8;

```
Qy        171 PRGGAVPRKPVSEMPMERDRGA----------------------------AHSLEPGKEN 202
              | ||: |  |     :: :||:                              |  |||:
Db        688 PAGGSGPAGPPGPQGVKGERGSPGGPGAAGFPGGRGPPGPPGSNGNPGPPGSSGAPGKDG 747

Qy        203 LPGDPTSNAT-----------------SRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGA 245
               || | ||                   ||| ||  ||  |   | ||     | |  |
Db        748 PPGPPGSNGAPGSPGISGPKGDSGPPGERGAPGPQGPPGAPGPLGIAG-----LTGARGL 802

Qy        246 GGAMCWRRRRAKP------SESRHPGP-------GSFGRGGSLGLGGGGGMGPREAEPGE 292
               |       |  |       |:  |||       |  |  |  || |  |   |:  ||
Db        803 AGPPGMPGARGSPGPQGIKGENGKPGPSGQNGERGPPGPQGLPGLAGTAGEPGRDGNPGS 862

Qy        293 LGIALRGG--------GAADPPFCPHYEKVSGDYGHPVYIVQDGPP 330
               |:  | |        |    |  |      |  |||      |||
Db        863 DGLPGRDGAPGAKGDRGENGSPGAP------GAPGHP------GPP 896
```

Search completed: April 13, 2004, 09:25:00
Job time : 20.4591 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 13, 2004, 09:26:02 ; Search time 42.9245 Seconds
(without alignments)
2787.142 Million cell updates/sec

Title: US-10-021-121-2
Perfect score: 2450
Sequence: 1 MGPPHSGPGGVRVGALLLLG.....TTLLRQRASVEAEAGQHGPL 455

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1073127 seqs, 262937947 residues

Total number of hits satisfying chosen parameters: 1073127

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description

1	2450	100.0	455	13	US-10-021-121-2	Sequence 2, Appli
2	1841	75.1	340	13	US-10-021-121-4	Sequence 4, Appli
3	1837	75.0	340	13	US-10-138-787-3	Sequence 3, Appli
4	1835	74.9	340	15	US-10-417-924A-2	Sequence 2, Appli
5	623	25.4	346	13	US-10-021-121-9	Sequence 9, Appli
6	623	25.4	346	16	US-10-356-289-2	Sequence 2, Appli
7	620.5	25.3	333	9	US-09-754-105-2	Sequence 2, Appli
8	620.5	25.3	333	9	US-09-978-339-2	Sequence 2, Appli
9	620.5	25.3	333	13	US-10-021-121-10	Sequence 10, Appl
10	620.5	25.3	333	15	US-10-331-496A-63	Sequence 63, Appl
11	613.5	25.0	333	13	US-10-138-787-4	Sequence 4, Appli
12	599.5	24.5	345	13	US-10-138-787-5	Sequence 5, Appli
13	489	20.0	89	9	US-09-862-179A-17	Sequence 17, Appl
14	489	20.0	89	13	US-10-138-787-13	Sequence 13, Appl
15	284.5	11.6	92	9	US-09-864-761-48262	Sequence 48262, A
16	196.5	8.0	136	9	US-09-864-761-48257	Sequence 48257, A
17	193.5	7.9	106	9	US-09-925-297-639	Sequence 639, App
18	192	7.8	82	9	US-09-862-179A-15	Sequence 15, Appl
19	192	7.8	82	13	US-10-138-787-11	Sequence 11, Appl
20	191.5	7.8	82	9	US-09-862-179A-16	Sequence 16, Appl
21	191.5	7.8	82	13	US-10-138-787-12	Sequence 12, Appl
22	179	7.3	238	9	US-09-904-954-2	Sequence 2, Appli
23	179	7.3	238	10	US-09-733-756-2	Sequence 2, Appli
24	179	7.3	238	14	US-10-241-220-72	Sequence 72, Appl
25	179	7.3	238	15	US-10-295-027-130	Sequence 130, App
26	176	7.2	209	9	US-09-921-984-2	Sequence 2, Appli
27	174.5	7.1	233	13	US-10-138-787-7	Sequence 7, Appli
28	172.5	7.0	218	9	US-09-925-297-510	Sequence 510, App
29	169.5	6.9	201	9	US-09-904-954-4	Sequence 4, Appli
30	169	6.9	201	13	US-10-138-787-8	Sequence 8, Appli
31	168.5	6.9	209	13	US-10-138-787-6	Sequence 6, Appli
32	167.5	6.8	228	8	US-08-578-684-4	Sequence 4, Appli
33	166	6.8	205	13	US-10-138-787-10	Sequence 10, Appl
34	166	6.8	205	14	US-10-171-311-50	Sequence 50, Appl
35	166	6.8	205	15	US-10-372-683-34	Sequence 34, Appl
36	164.5	6.7	204	12	US-10-147-493-288	Sequence 288, App
37	164.5	6.7	204	12	US-10-145-127-288	Sequence 288, App
38	164.5	6.7	204	12	US-10-160-503-288	Sequence 288, App
39	164.5	6.7	204	12	US-10-143-118-288	Sequence 288, App
40	164.5	6.7	204	12	US-10-144-993-288	Sequence 288, App
41	164.5	6.7	204	12	US-10-158-787-288	Sequence 288, App
42	164.5	6.7	204	12	US-10-140-024-288	Sequence 288, App
43	164.5	6.7	204	13	US-10-001-054-48	Sequence 48, Appl
44	164.5	6.7	204	14	US-10-028-072-288	Sequence 288, App
45	164.5	6.7	204	14	US-10-121-049-288	Sequence 288, App

ALIGNMENTS

RESULT 1
US-10-021-121-2
; Sequence 2, Application US/10021121
; Publication No. US20020142444A1
; GENERAL INFORMATION:
; APPLICANT: Caras, Ingrid W

```
;         TITLE OF INVENTION: A2-1 Neurotrophic Factor
;         NUMBER OF SEQUENCES: 10
;         CORRESPONDENCE ADDRESS:
;              ADDRESSEE: Genentech, Inc.
;              STREET: 1 DNA Way
;              CITY: South San Francisco
;              STATE: California
;              COUNTRY: USA
;              ZIP: 94080
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;              COMPUTER: IBM PC compatible
;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: WinPatin (Genentech)
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/10/021,121
;              FILING DATE: 06-Dec-2001
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: US/08/635,130
;              FILING DATE: 19-Mar-1996
;         ATTORNEY/AGENT INFORMATION:
;              NAME: Torchia, PhD., Timothy E.
;              REGISTRATION NUMBER: 36,700
;              REFERENCE/DOCKET NUMBER: P1001
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: 650/225-8674
;              TELEFAX: 650/952-9881
;    INFORMATION FOR SEQ ID NO: 2:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 455 amino acids
;              TYPE: Amino Acid
;              TOPOLOGY: Linear
;         SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-021-121-2

  Query Match             100.0%;  Score 2450;  DB 13;  Length 455;
  Best Local Similarity   100.0%;  Pred. No. 8.5e-187;
  Matches  455;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

Qy         61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy        121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180

Qy        181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

Qy        241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300

Qy        301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYTSISVLEWPILHTIQLFFMRSK 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYTSISVLEWPILHTIQLFFMRSK 360

Qy        361 CSRVTTFLFPVQVITTSTCRMTSFSFTTLNPSMQACRAQMGEFRIRWCFWGDRILGTALF 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CSRVTTFLFPVQVITTSTCRMTSFSFTTLNPSMQACRAQMGEFRIRWCFWGDRILGTALF 420

Qy        421 VLVLILLLGRLNMHQTTLLRQRASVEAEAGQHGPL 455
                |||||||||||||||||||||||||||||||||||
Db        421 VLVLILLLGRLNMHQTTLLRQRASVEAEAGQHGPL 455


RESULT 2
US-10-021-121-4
; Sequence 4, Application US/10021121
; Publication No. US20020142444A1
;   GENERAL INFORMATION:
;        APPLICANT: Caras, Ingrid W
;        TITLE OF INVENTION: A2-1 Neurotrophic Factor
;        NUMBER OF SEQUENCES: 10
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Genentech, Inc.
;             STREET: 1 DNA Way
;             CITY: South San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94080
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: WinPatin (Genentech)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/021,121
;             FILING DATE: 06-Dec-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/635,130
;             FILING DATE: 19-Mar-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Torchia, PhD., Timothy E.
;             REGISTRATION NUMBER: 36,700
;             REFERENCE/DOCKET NUMBER: P1001
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650/225-8674
;             TELEFAX: 650/952-9881
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 340 amino acids
;             TYPE: Amino Acid
;             TOPOLOGY: Linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-021-121-4
```

Query Match 75.1%; Score 1841; DB 13; Length 340;
Best Local Similarity 100.0%; Pred. No. 2e-138;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

Qy         61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy        121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180

Qy        181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

Qy        241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300

Qy        301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
              ||||||||||||||||||||||||||||||||||||||
Db        301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
```

RESULT 3
US-10-138-787-3
; Sequence 3, Application US/10138787
; Publication No. US20020172984A1
; GENERAL INFORMATION:
; APPLICANT: Holland, Sacha
; APPLICANT: Mbamalu, Geraldine
; APPLICANT: Pawson, Tony
; TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
; TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
; TITLE OF INVENTION: TYROSINE KINASES
; FILE REFERENCE: 11757.23USWO
; CURRENT APPLICATION NUMBER: US/10/138,787
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US/09/214,631
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: PCT/CA97/00473
; PRIOR FILING DATE: 1997-07-04
; PRIOR APPLICATION NUMBER: 60/021,272
; PRIOR FILING DATE: 1996-07-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-138-787-3

```
  Query Match             75.0%;  Score 1837;  DB 13;  Length 340;
  Best Local Similarity   99.7%;  Pred. No. 4.2e-138;
  Matches  337;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

Qy         61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy        121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
              ||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||
Db        121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLQVGQSPRGGAVPRKP 180

Qy        181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

Qy        241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300

Qy        301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
              ||||||||||||||||||||||||||||||||||||||
Db        301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338


RESULT 4
US-10-417-924A-2
; Sequence 2, Application US/10417924A
; Publication No. US20030215918A1
; GENERAL INFORMATION:
;  APPLICANT: Samuel Davis, et al.
;  TITLE OF INVENTION: BIOLOGICALLY ACTIVE EPH FAMILY LIGANDS
;  FILE REFERENCE: REG-341Z
;  CURRENT APPLICATION NUMBER: US/10/417,924A
;  CURRENT FILING DATE:  2003-04-17
;  PRIOR APPLICATION NUMBER: 09/051,994
;  PRIOR FILING DATE: 1998-04-24
;  PRIOR APPLICATION NUMBER: PCT/US96/17201
;  PRIOR FILING DATE: 1996-10-25
;  PRIOR APPLICATION NUMBER: 60/007,015
;  PRIOR FILING DATE: 1995-10-25
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 340
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: Misc. feature
;   LOCATION: (166)
;   OTHER INFORMATION: Xaa = unknown or other
US-10-417-924A-2
```

```
  Query Match             74.9%;  Score 1835;  DB 15;  Length 340;
  Best Local Similarity   99.7%;  Pred. No. 6e-138;
  Matches  337;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

Qy         61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy        121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLXVGQSPRGGAVPRKP 180

Qy        181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

Qy        241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300

Qy        301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
              ||||||||||||||||||||||||||||||||||||||
Db        301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338


RESULT 5
US-10-021-121-9
; Sequence 9, Application US/10021121
; Publication No. US20020142444A1
;   GENERAL INFORMATION:
;        APPLICANT: Caras, Ingrid W
;        TITLE OF INVENTION: A2-1 Neurotrophic Factor
;        NUMBER OF SEQUENCES: 10
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Genentech, Inc.
;             STREET: 1 DNA Way
;             CITY: South San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94080
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: WinPatin (Genentech)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/021,121
;             FILING DATE: 06-Dec-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/635,130
;             FILING DATE: 19-Mar-1996
```

```
;         ATTORNEY/AGENT INFORMATION:
;              NAME: Torchia, PhD., Timothy E.
;              REGISTRATION NUMBER: 36,700
;              REFERENCE/DOCKET NUMBER: P1001
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: 650/225-8674
;              TELEFAX: 650/952-9881
;    INFORMATION FOR SEQ ID NO: 9:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 346 amino acids
;              TYPE: Amino Acid
;              TOPOLOGY: Linear
;         SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-021-121-9

  Query Match             25.4%;  Score 623;  DB 13;  Length 346;
  Best Local Similarity   39.2%;  Pred. No. 2.4e-41;
  Matches  143;  Conservative   48;  Mismatches  116;  Indels   58;  Gaps    9;

Qy          8 PGGVRVGALLLLGVLGLVSGL------SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
              ||   :|  |:  |:  :  |      :|||| |:| | :| :  | |:||:|||:||::
Db          4 PGQRWLGKWLVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63

Qy         62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
              ||||    |     ||:||||||   |   |     ||:|:||:||: ::|||||||:|
Db         64 CPRAEAGRP-----YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118

Qy        122 PNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
              ||  | ||: |||||| :||:|: ||||: :|||| || ||::::||| |      :
Db        119 PNYMGLEFKKHHDYYITSTSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTT 178

Qy        182 SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
              |    | |     : : ||     ||      :   |    |       ||:|| :
Db        179 SRPSKEADNTVKMATQAPGSRGSLGDSDGKHETVNQEEKSGP-------GASGGSSGDPD 231

Qy        237 ------LLLLGVAGAGGA-------------MCWRRRRAKPSESRHPGPGSFGRGGSLGL 277
                    : |    |||                :  |:|  | ::          |  :| |
Db        232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLKLRKRHRKHTQQ---------RAAALSL 282

Qy        278 ----GGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
                   || |    || :: | ||     :  :||||||||||||||||||: |||||
Db        283 STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP 339

Qy        334 PNIYY 338
               ||||
Db        340 ANIYY 344


RESULT 6
US-10-356-289-2
; Sequence 2, Application US/10356289
; Publication No. US20040022767A1
; GENERAL INFORMATION:
;  APPLICANT: Lyman, Stewart D.
;  APPLICANT:  Beckmann, M. Patricia
;  APPLICANT:  Baum, Peter R.
;  APPLICANT:  Carpenter, Melissa K.
```

```
;  TITLE OF INVENTION: NOVEL CYTOKINE DESIGNATED ELK LIGAND
;  FILE REFERENCE: GENENT.67CPDV3
;  CURRENT APPLICATION NUMBER: US/10/356,289
;  CURRENT FILING DATE:  2003-01-31
;  PRIOR APPLICATION NUMBER: US/09/039,642B
;  PRIOR FILING DATE: 1998-03-16
;  PRIOR APPLICATION NUMBER: 08/213,403
;  PRIOR FILING DATE: 1994-03-15
;  PRIOR APPLICATION NUMBER: 07/977,693
;  PRIOR FILING DATE: 1992-11-13
;  PRIOR APPLICATION NUMBER: 08/747,240
;  PRIOR FILING DATE: 1996-10-12
;  PRIOR APPLICATION NUMBER: 08/460,741
;  PRIOR FILING DATE: 1995-06-02
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 346
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-356-289-2

  Query Match             25.4%;  Score 623;  DB 16;  Length 346;
  Best Local Similarity   39.2%;  Pred. No. 2.4e-41;
  Matches  143;  Conservative   48;  Mismatches  116;  Indels   58;  Gaps    9;

Qy          8 PGGVRVGALLLLGVLGLVSGL------SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
              ||   :|  |:  |:  :  |      :|||| |:| | :| :  | |:||:|||:||:: 
Db          4 PGQRWLGKWLVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63

Qy         62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
              ||||    |     ||:||||||   |   |     ||:|:||:||: ::|||||||:| 
Db         64 CPRAEAGRP-----YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118

Qy        122 PNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
              ||  | ||: |||||| :||:|: |||||: :|||| || ||::::||| |      : 
Db        119 PNYMGLEFKKHHDYYITSTSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTT 178

Qy        182 SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
              |    | |     : : ||     ||      :   |    |       ||:|| :     
Db        179 SRPSKEADNTVKMATQAPGSRGSLGDSDGKHETVNQEEKSGP-------GASGGSSGDPD 231

Qy        237 ------LLLLGVAGAGGA------------MCWRRRRAKPSESRHPGPGSFGRGGSLGL 277
                    : |    |||               :  |:|  | ::          |  :| | 
Db        232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLKLRKRHRKHTQQ---------RAAALSL 282

Qy        278 ----GGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
                  || |    || :: | ||     :  :|||||||||||||||||: |||||     
Db        283 STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP 339

Qy        334 PNIYY 338
               ||||
Db        340 ANIYY 344


RESULT 7
US-09-754-105-2
```

; Sequence 2, Application US/09754105
; Patent No. US20010009768A1
; GENERAL INFORMATION:
; APPLICANT: Cerretti, Douglas
; APPLICANT: Reddy, Pranhitha
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING CYTOKINE DESIGNATED LERK-5
; FILE REFERENCE: 28232
; CURRENT APPLICATION NUMBER: US/09/754,105
; CURRENT FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: 09/329,531
; PRIOR FILING DATE: 1999-06-10
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
;   LENGTH: 333
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-09-754-105-2

  Query Match   25.3%; Score 620.5; DB 9; Length 333;
  Best Local Similarity   40.5%; Pred. No. 3.5e-41;
  Matches 133; Conservative   52; Mismatches 130; Indels   13; Gaps   5;

```
Qy          14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
               | |::|    :   : |||:||||:| :|    | |||||||||::||::||:       :
Db          14 GVLMVLCRTAISKSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 70

Qy          74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
                 ||:||:|:|   |  ||        || | :|| |::|||||||:|||||| ||: :
Db          71 GQYEYYKVYMVDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK 130

Qy         134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
               |||||:||:|: |||:: :|||| || ||:|::|||  |  |    : |     :|
Db         131 DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN 190

Qy         191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
               | : :  |  :  ||  |   ::  :   :    :   || | |  : :: :      :
Db         191 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLL 250

Qy         251 WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
                 ||| :    :|    |     :    |        :|| :: | ||    ||  ||||
Db         251 KYRRRHRKHSPQHTTTLSLSTLATPKRSGNN----NGSEPSDIIIPLR---TADSVFCPH 303

Qy         311 YEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
               ||||||||||||||: ||||| ||||
Db         304 YEKVSGDYGHPVYIVQEMPPQSPANIYY 331
```

RESULT 8
US-09-978-339-2
; Sequence 2, Application US/09978339
; Patent No. US20020103358A1
;   GENERAL INFORMATION:
;   APPLICANT: Cerretti, Douglas P.
;   Reddy, Pranhitha
;   TITLE OF INVENTION: No. US20020103358A1el Cytokine Designated Lerk-5
;   NUMBER OF SEQUENCES: 3

```
;         CORRESPONDENCE ADDRESS:
;              ADDRESSEE: Immunex Corporation
;              STREET: 51 University Street
;              CITY: Seattle
;              STATE: Washington
;              COUNTRY: US
;              ZIP: 98101
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: Floppy disk
;              COMPUTER: Apple Macintosh
;              OPERATING SYSTEM: Apple 7.1
;              SOFTWARE: Microsoft Word, Version 5.1a
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/09/978,339
;              FILING DATE: 15-Oct-2001
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: 08/271,948
;              FILING DATE: <Unknown>
;         ATTORNEY/AGENT INFORMATION:
;              NAME: Seese, Kathryn A.
;              REGISTRATION NUMBER: 32,172
;              REFERENCE/DOCKET NUMBER: 2823
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (206) 587-0430
;              TELEFAX: (206) 233-0644
;              TELEX: 756822
;    INFORMATION FOR SEQ ID NO: 2:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 333 amino acids
;              TYPE: amino acid
;              TOPOLOGY: linear
;         MOLECULE TYPE: protein
;         SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-978-339-2

  Query Match             25.3%;  Score 620.5;  DB 9;  Length 333;
  Best Local Similarity   40.5%;  Pred. No. 3.5e-41;
  Matches  133;  Conservative   52;  Mismatches  130;  Indels   13;  Gaps    5;

Qy         14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
              | |::|    :   : |||:||||:| :|    | ||||||||:||::||:       :
Db         14 GVLMVLCRTAISKSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 70

Qy         74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
               ||:||:|:|   |  ||        || | :|| |::||||||:|||||| ||: :
Db         71 GQYEYYKVYMVDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK 130

Qy        134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
              |||||:||:|: |||:: :|||| || ||:|::|||  |  |    : |     :|
Db        131 DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN 190

Qy        191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
              | : :  |  :  ||  |   ::  :   :    :   || | |  : :: :      :
Db        191 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLL 250

Qy        251 WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
```

```
              ||| :    :|    |     :    |        :|| :: | ||    ||  ||||
Db        251 KYRRRHRKHSPQHTTTLSLSTLATPKRSGNN----NGSEPSDIIIPLR---TADSVFCPH 303

Qy        311 YEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
              ||||||||||||||||: ||||| ||||
Db        304 YEKVSGDYGHPVYIVQEMPPQSPANIYY 331


RESULT 9
US-10-021-121-10
; Sequence 10, Application US/10021121
; Publication No. US20020142444A1
;   GENERAL INFORMATION:
;        APPLICANT: Caras, Ingrid W
;        TITLE OF INVENTION: A2-1 Neurotrophic Factor
;        NUMBER OF SEQUENCES: 10
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Genentech, Inc.
;             STREET: 1 DNA Way
;             CITY: South San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94080
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: WinPatin (Genentech)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/021,121
;             FILING DATE: 06-Dec-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/635,130
;             FILING DATE: 19-Mar-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Torchia, PhD., Timothy E.
;             REGISTRATION NUMBER: 36,700
;             REFERENCE/DOCKET NUMBER: P1001
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650/225-8674
;             TELEFAX: 650/952-9881
;   INFORMATION FOR SEQ ID NO: 10:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 333 amino acids
;             TYPE: Amino Acid
;             TOPOLOGY: Linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-021-121-10

  Query Match            25.3%;  Score 620.5;  DB 13;  Length 333;
  Best Local Similarity  40.5%;  Pred. No. 3.5e-41;
  Matches  133;  Conservative   52;  Mismatches  130;  Indels   13;  Gaps    5;

Qy         14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
              | |::|    :   : |||:||||:| :|    | |||||||||:||::||:       :
Db         14 GVLMVLCRTAISKSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 70
```

```
Qy          74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
               ||:|||:|:|   |  ||        || | :|| |:::|||||||:|||||| ||: :
Db          71 GQYEYYKVYMVDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK 130

Qy         134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
               |||||:||:|: |||:: :|||| || ||:|::|||  |  |    : |     :|
Db         131 DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN 190

Qy         191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
               | : :  |  :  ||  |   ::  :   :    :   || | |  : :: :      :
Db         191 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLL 250

Qy         251 WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
               |||  :    :|    |     :    |        :|| :: | ||    ||  ||||
Db         251 KYRRRHRKHSPQHTTTLSLSTLATPKRSGNN----NGSEPSDIIIPLR---TADSVFCPH 303

Qy         311 YEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
               ||||||||||||||: ||||| ||||
Db         304 YEKVSGDYGHPVYIVQEMPPQSPANIYY 331
```

RESULT 10
US-10-331-496A-63
; Sequence 63, Application US/10331496A
; Publication No. US20030228305A1
; GENERAL INFORMATION:
; APPLICANT: FRANTZ,GRETCHEN
; APPLICANT: HILLAN,KENNETH J.
; APPLICANT: PHILLIPS,HEIDI S.
; APPLICANT: POLAKIS,PAUL
; APPLICANT: SMITH,VICTORIA
; APPLICANT: SPENCER,SUSAN D.
; APPLICANT: WILLIAMS,P. MICKEY
; APPLICANT: WU,THOMAS D.
; APPLICANT: ZHANG,ZEMIN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5014R1-PCT
; CURRENT APPLICATION NUMBER: US/10/331,496A
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 60/345,444
; PRIOR FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: US 60/351,885
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 60/360,066
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: US 60/362,004
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/366,869
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: US 60/366,284
; PRIOR FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: US 60/368,679
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FILING DATE: 2002-08-19

; PRIOR APPLICATION NUMBER: US 60/405,645
; PRIOR FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 95
; SEQ ID NO 63
;   LENGTH: 333
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-10-331-496A-63

  Query Match   25.3%; Score 620.5; DB 15; Length 333;
  Best Local Similarity   40.5%; Pred. No. 3.5e-41;
  Matches 133; Conservative   52; Mismatches 130; Indels   13; Gaps   5;

```
Qy         14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
              | |:::|    :   : |||:||||:| :|    | |||||||||:||::||:       :
Db         14 GVLMVLCRTAISKSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 70

Qy         74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
                ||:||:|:|   |  ||        || | :|| |::|||||||:|||||| ||: :
Db         71 GQYEYYKVYMVDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK 130

Qy        134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
              |||||:||:|: |||:: :|||| || ||:|::|||  |  |    : |     :|
Db        131 DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN 190

Qy        191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
              | : :  |  : ||  |   ::  :   :    :   || | |  : :: :      :
Db        191 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLL 250

Qy        251 WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
                ||| :    :|    |     :    |        :|| :: | ||    ||  ||||
Db        251 KYRRRHRKHSPQHTTTLSLSTLATPKRSGNN----NGSEPSDIIIPLR---TADSVFCPH 303

Qy        311 YEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
              |||||||||||||||: ||||| ||||
Db        304 YEKVSGDYGHPVYIVQEMPPQSPANIYY 331
```

RESULT 11
US-10-138-787-4
; Sequence 4, Application US/10138787
; Publication No. US20020172984A1
; GENERAL INFORMATION:
; APPLICANT: Holland, Sacha
; APPLICANT: Mbamalu, Geraldine
; APPLICANT: Pawson, Tony
; TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
; TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
; TITLE OF INVENTION: TYROSINE KINASES
; FILE REFERENCE: 11757.23USWO
; CURRENT APPLICATION NUMBER: US/10/138,787
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US/09/214,631
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: PCT/CA97/00473
; PRIOR FILING DATE: 1997-07-04
; PRIOR APPLICATION NUMBER: 60/021,272

```
;  PRIOR FILING DATE: 1996-07-05
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 333
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-138-787-4

  Query Match             25.0%;  Score 613.5;  DB 13;  Length 333;
  Best Local Similarity   40.5%;  Pred. No. 1.3e-40;
  Matches  133;  Conservative   54;  Mismatches  128;  Indels   13;  Gaps    6;

Qy         14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
              | |::|    :   : |||:| ||:| :|    | ||||||||:||::||:       :
Db         14 GVLMVLCRTAISKSIVLEPIYMNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 70

Qy         74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
                ||:||:|:|   |  ||        || | :|| |::|||||||:|||||| ||: :
Db         71 GQYEYYKVYMVDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK 130

Qy        134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ-SPRGGAVPRKPVSEMP-MER-DR 190
              |||||:||:|: |||:: :|||| || ||:|::||| :   |: | |  :  | :|
Db        131 DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTPNKDPTRRPELEAGTN 190

Qy        191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
              | : :  |  :  ||  |   ::  :   :    :   || | |  : :: :      :
Db        191 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLL 250

Qy        251 WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
                ||| :    :|    |     :    |        :|| :: | ||    ||  ||||
Db        251 KYRRRHRKHSPQHTTTLSLSTLATPKRSGNN----NGSEPSDIIIPLR---TADSVFCPH 303

Qy        311 YEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
              ||||||||||||||||: ||||| ||||
Db        304 YEKVSGDYGHPVYIVQEMPPQSPANIYY 331


RESULT 12
US-10-138-787-5
; Sequence 5, Application US/10138787
; Publication No. US20020172984A1
; GENERAL INFORMATION:
;  APPLICANT: Holland, Sacha
;  APPLICANT:  Mbamalu, Geraldine
;  APPLICANT:  Pawson, Tony
;  TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
;  TITLE OF INVENTION:  BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
;  TITLE OF INVENTION:  TYROSINE KINASES
;  FILE REFERENCE: 11757.23USWO
;  CURRENT APPLICATION NUMBER: US/10/138,787
;  CURRENT FILING DATE:  2002-05-03
;  PRIOR APPLICATION NUMBER: US/09/214,631
;  PRIOR FILING DATE: 1999-03-12
;  PRIOR APPLICATION NUMBER: PCT/CA97/00473
;  PRIOR FILING DATE: 1997-07-04
;  PRIOR APPLICATION NUMBER: 60/021,272
```

```
;  PRIOR FILING DATE: 1996-07-05
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 345
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-138-787-5

  Query Match             24.5%;  Score 599.5;  DB 13;  Length 345;
  Best Local Similarity   38.4%;  Pred. No. 1.7e-39;
  Matches  140;  Conservative   50;  Mismatches  116;  Indels   59;  Gaps   10;

Qy          8 PGGVRVG----ALLLLGVLGLVSGL--SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
              |||  :|    |:::  :  | : |  :|||| |:| | :| :  | |:||:|||:||::
Db          4 PGGRWLGKWLYAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63

Qy         62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
              || |    |     ||:||||||   |   |     | :|:||:||: ::|||||||:|
Db         64 CPPAEAGRP-----YEYYKLYLVRPEQAAACSTVLDPMVLVTCNRPEQEIRFTIKFQEFS 118

Qy        122 PNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
              ||  | ||: |||||| :||:|: |||| : :|||| || ||:::::||| |      :
Db        119 PNYMGLEFKKHHDYYITSTSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTT 178

Qy        182 SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
              |    | |     : : ||     ||      :   |    |       ||:|| :
Db        179 SRPSKEADNTVKMATQAPGSRGSLGDSDGKHETVNQEEKSGP-------GASGGSSGDPD 231

Qy        237 ------LLLLGVAGAGGA-------------MCWRRRRAKPSESRHPGPGSFGRGGSLGL 277
                    : |    |||                :   :|  | ::          |  :| |
Db        232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLKLPKRHRKHTQ----------RAAALSL 281

Qy        278 ----GGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
                  || |    || :: | |      :  :|||||||||||||||||||: |||||
Db        282 STIASPKGGSGTAGTEPSDIIIPL---FTTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP 338

Qy        334 PNIYY 338
               ||||
Db        339 ANIYY 343


RESULT 13
US-09-862-179A-17
; Sequence 17, Application US/09862179A
; Patent No. US20020147306A1
; GENERAL INFORMATION:
;  APPLICANT: Lin, Danny
;  APPLICANT:  Pawson, Anthony
;  TITLE OF INVENTION: PEPTIDES THAT MODULATE THE INTERACTION OF B CLASS EPHRINS
;  TITLE OF INVENTION:  AND PDZ DOMAINS
;  FILE REFERENCE: MTSI-P01-009
;  CURRENT APPLICATION NUMBER: US/09/862,179A
;  CURRENT FILING DATE:  2001-05-21
;  NUMBER OF SEQ ID NOS: 44
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
```

```
;   LENGTH: 89
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-862-179A-17

  Query Match             20.0%;  Score 489;  DB 9;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 2e-31;
  Matches   87;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        252 RRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPHY 311
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 RRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPHY 60

Qy        312 EKVSGDYGHPVYIVQDGPPQSPPNIYY 338
              |||||||||||||||||||||||||||
Db         61 EKVSGDYGHPVYIVQDGPPQSPPNIYY 87


RESULT 14
US-10-138-787-13
; Sequence 13, Application US/10138787
; Publication No. US20020172984A1
; GENERAL INFORMATION:
;  APPLICANT: Holland, Sacha
;  APPLICANT:  Mbamalu, Geraldine
;  APPLICANT:  Pawson, Tony
;  TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
;  TITLE OF INVENTION:  BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
;  TITLE OF INVENTION:  TYROSINE KINASES
;  FILE REFERENCE: 11757.23USWO
;  CURRENT APPLICATION NUMBER: US/10/138,787
;  CURRENT FILING DATE:  2002-05-03
;  PRIOR APPLICATION NUMBER: US/09/214,631
;  PRIOR FILING DATE: 1999-03-12
;  PRIOR APPLICATION NUMBER: PCT/CA97/00473
;  PRIOR FILING DATE: 1997-07-04
;  PRIOR APPLICATION NUMBER: 60/021,272
;  PRIOR FILING DATE: 1996-07-05
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
;   LENGTH: 89
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-138-787-13

  Query Match             20.0%;  Score 489;  DB 13;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 2e-31;
  Matches   87;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        252 RRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPHY 311
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 RRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPHY 60

Qy        312 EKVSGDYGHPVYIVQDGPPQSPPNIYY 338
              |||||||||||||||||||||||||||
Db         61 EKVSGDYGHPVYIVQDGPPQSPPNIYY 87
```

RESULT 15
US-09-864-761-48262
; Sequence 48262, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 48262
; LENGTH: 92

; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL136092.7
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.9
; OTHER INFORMATION: SWISSPROT HIT: P98172, EVALUE 4.00e-51
; OTHER INFORMATION: EST_HUMAN HIT: BE562822.1, EVALUE 3.00e-50
US-09-864-761-48262

  Query Match   11.6%; Score 284.5; DB 9; Length 92;
  Best Local Similarity   54.2%; Pred. No. 4.2e-15;
  Matches   52; Conservative   15; Mismatches   24; Indels   5; Gaps   1;

```
Qy          42 FQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLL 101
               | :  | |:||:|||:||::||||    |     ||:||||||   |   |     ||:|
Db           1 FLSGKGLVIYPKIGDKLDIICPRAEAGRP-----YEYYKLYLVRPEQAAACSTVLDPNVL 55

Qy         102 LTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYI 137
               :||:||: ::|||||||||:|||  | ||: ||||||
Db          56 VTCNRPEQEIRFTIKFQEFSPNYMGLEFKKHHDYYI 91
```

Search completed: April 13, 2004, 09:39:50
Job time : 43.9245 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 13, 2004, 09:22:17 ; Search time 66.9623 Seconds
(without alignments)
2143.906 Million cell updates/sec

Title: US-10-021-121-2
Perfect score: 2450
Sequence: 1 MGPPHSGPGGVRVGALLLLG.....TTLLRQRASVEAEAGQHGPL 455

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description

1	914	37.3	331	13	Q90Z31	Q90z31 brachydanio
2	910	37.1	327	13	Q9PT69	Q9pt69 xenopus lae
3	620.5	25.3	333	13	Q9PUJ4	Q9puj4 gallus gall
4	607	24.8	341	13	Q90Z33	Q90z33 brachydanio
5	596.5	24.3	334	13	Q90Z32	Q90z32 brachydanio
6	331	13.5	205	13	Q9W6H9	Q9w6h9 xenopus lae
7	214.5	8.8	237	5	Q9U3M2	Q9u3m2 caenorhabdi
8	198.5	8.1	279	5	Q9U474	Q9u474 caenorhabdi
9	192	7.8	652	5	Q9V4E1	Q9v4e1 drosophila
10	178.5	7.3	202	13	Q98TZ1	Q98tz1 gallus gall
11	168.5	6.9	205	4	Q8N578	Q8n578 homo sapien
12	167	6.8	205	11	Q9D7K8	Q9d7k8 mus musculu
13	163.5	6.7	206	11	Q9CZS8	Q9czs8 mus musculu
14	155.5	6.3	675	6	Q9N178	Q9n178 sus scrofa
15	155	6.3	229	13	O93431	O93431 brachydanio
16	153.5	6.3	217	13	Q7SY61	Q7sy61 xenopus lae
17	153.5	6.3	1691	11	Q9ESQ2	Q9esq2 mus musculu
18	151.5	6.2	1447	13	Q9IB91	Q9ib91 xenopus lae
19	150	6.1	2936	6	Q7YRK8	Q7yrk8 canis famil
20	149	6.1	325	5	O17036	O17036 caenorhabdi
21	149	6.1	569	5	Q17208	Q17208 bombyx mori
22	148.5	6.1	316	5	Q19111	Q19111 caenorhabdi
23	147	6.0	921	11	Q8BSQ4	Q8bsq4 mus musculu
24	146.5	6.0	590	5	Q86BH0	Q86bh0 drosophila
25	146.5	6.0	778	5	Q86BH1	Q86bh1 drosophila
26	146.5	6.0	792	5	Q8MT89	Q8mt89 drosophila
27	146.5	6.0	888	11	Q8CCZ8	Q8ccz8 mus musculu
28	146.5	6.0	1140	11	Q61434	Q61434 mus musculu
29	146.5	6.0	1449	13	Q802B5	Q802b5 xenopus lae
30	146.5	6.0	1491	13	Q91718	Q91718 xenopus lae
31	146.5	6.0	1491	13	Q7ZTM4	Q7ztm4 xenopus lae
32	146	6.0	675	13	Q90800	Q90800 gallus gall
33	146	6.0	1669	11	Q9QZS0	Q9qzs0 mus musculu
34	145.5	5.9	305	5	O17805	O17805 caenorhabdi
35	145.5	5.9	308	5	Q94620	Q94620 meloidogyne
36	145	5.9	680	11	Q9D0D2	Q9d0d2 mus musculu
37	144.5	5.9	309	5	Q25466	Q25466 meloidogyne
38	144.5	5.9	1269	13	Q7T2Z7	Q7t2z7 gallus gall
39	144.5	5.9	1347	4	Q96QB3	Q96qb3 homo sapien
40	144.5	5.9	1420	13	Q90W37	Q90w37 gallus gall
41	143.5	5.9	775	16	Q9F342	Q9f342 streptomyce
42	143	5.8	445	5	Q8MZ49	Q8mz49 drosophila
43	143	5.8	1684	6	Q8HYC1	Q8hyc1 canis famil
44	143	5.8	1688	6	Q866Z2	Q866z2 canis famil
45	143	5.8	1747	5	Q26640	Q26640 strongyloce

ALIGNMENTS

```
RESULT 1
Q90Z31
ID   Q90Z31      PRELIMINARY;      PRT;   331 AA.
AC   Q90Z31;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
```

```
DE   Ephrin B3.
GN   EFNB3.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21290827; PubMed=11397014;
RA   Chan J., Mably J.D., Serluca F.C., Chen J.N., Goldstein N.B.,
RA   Thomas M.C., Cleary J.A., Brennan C., Fishman M.C., Roberts T.M.;
RT   "Morphogenesis of prechordal plate and notochord requires intact
RT   eph/ephrin b signaling.";
RL   Dev. Biol. 234:470-482(2001).
DR   EMBL; AF375227; AAK64277.1; -.
DR   ZFIN; ZDB-GENE-010618-3; efnb3.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008972; Cupredoxin.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
SQ   SEQUENCE   331 AA;  35638 MW;  6A5EACD509A09818 CRC64;

  Query Match             37.3%;  Score 914;  DB 13;  Length 331;
  Best Local Similarity   54.5%;  Pred. No. 1.3e-64;
  Matches  188;  Conservative   43;  Mismatches   74;  Indels   40;  Gaps   10;

Qy         10 GVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPG 69
              |: :  : |: :|| ::  ::||:|||| |||| : ||||||||||||||:|| : |||
Db          9 GLGILLIFLVDLLG-ITATNMEPIYWNSLNKRFSDDKGYVLYPQIGDRLDLICPSSDPPG 67

Qy         70 PHSSPNYEFYKLYLVGG-AQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHE 128
              | :  :||:||||||    |  |||   |||||||||:|: |:||||||||||||||||
Db         68 PRAPADYEYYKLYLVSSREQADRCEVTGAPNLLLTCDKPNSDMRFTIKFQEYSPNLWGHE 127

Qy        129 FRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRG-GAVPRKPVSEMPME 187
              |:::|||:|||||||||:||||::|||| |:||||:|:|||||  |   |    || |
Db        128 FKTNHDYFIIATSDGTRQGLESMRGGVCATQGMKVVLKVGQSPYGLPAKSPKPDS----- 182

Qy        188 RDRGAAHSLEPGKENLPGDPTSNAT--------SRGAEGPLPPPSMPAVAGAAGGLALLL 239
                        |: | |   | |:|        | |  ||||  ::  :||||||  | ||
Db        183 ----------AGRINNPNPGTGNSTHPQIPPRGSGGENGPLPASNIAVIAGAAGGSAFLL 232

Qy        240 LGVAGAGGAMCWRRRRAKPSESRHPGPGSFG------RGGSLGLGGGGGMGPREAEPGEL 293
              | |      :|:||| || ||| || | |         ||   |:|||   |   :|| ::
Db        233 L-VTAVICVVCYRRRHAKHSESHHP-PLSLSSLTSPKRGCGGGVGGGNNNG---SEPSDI 287

Qy        294 GIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
               | ||    :|  :|||||||||||||||||: ||||| ||||
Db        288 IIPLR---TSDSAYCPHYEKVSGDYGHPVYIVQEMPPQSPANIYY 329


RESULT 2
Q9PT69
```

```
ID   Q9PT69      PRELIMINARY;      PRT;   327 AA.
AC   Q9PT69;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Ephrin-B3 precursor.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=20099673; PubMed=10633856;
RA   Helbling P.M., Saulnier D.M.E., Robinson V., Christiansen J.H.,
RA   Wilkinson D.G., Brandli A.W.;
RT   "Comparative analysis of embryonic gene expression defines potential
RT   interaction sites for Xenopus EphB4 receptors with ephrin-B ligands.";
RL   Dev. Dyn. 216:361-373(1999).
DR   EMBL; AJ236866; CAB65511.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0016491; F:oxidoreductase activity; IEA.
DR   GO; GO:0008152; P:metabolism; IEA.
DR   InterPro; IPR002086; Aldehyde_dehydr.
DR   InterPro; IPR008972; Cupredoxin.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Signal.
FT   SIGNAL        1     24       POTENTIAL.
SQ   SEQUENCE   327 AA;  35913 MW;  4BB0FA39D4C22DCD CRC64;

  Query Match             37.1%;  Score 910;  DB 13;  Length 327;
  Best Local Similarity   60.1%;  Pred. No. 2.6e-64;
  Matches  190;  Conservative   30;  Mismatches   82;  Indels   14;  Gaps    8;

Qy         25 VSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLV 84
              :| |||:|:||||:||||:   |||||||||||||||||: | || ||  ||:||||||
Db         22 ISALSLDPIYWNSSNKRFEDTEGYVLYPQIGDRLDLLCPRSEPQGPFSSSPYEYYKLYLV 81

Qy         85 GGAQG-RRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDG 143
              |  :    |     |||||||||  ||||||||||:|||||||||:|  ||||||||||
Db         82 GTKEEMSSCSILRTPNLLLTCDRPSQDLRFTIKFQEFSPNLWGHEFQSQRDYYIIATSDG 141

Qy        144 TREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSL-EPGKEN 202
              | :|:|:|||||| |:|||| |:||||| |   ||:| |     :| | : |:  |   |
Db        142 TMDGIETLQGGVCETKGMKVTLKVGQSPNGATPPRRPSS---AGKDSGISPSVPNPDIPN 198

Qy        203 LPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMCWRRRRAKPSESR 262
              : |: : |||  |  ||||   :| |||||| ||||| | |  | :| |||:|| |::|
Db        199 V-GETSGNATKTGENGPLPISHVPLVAGAAGGAALLLL-VFGVVGWVCHRRRQAKHSDTR 256

Qy        263 HPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPV 322
```

```
              || | | |   |   ||         || :: : ||   |    ||||||||||||||||
Db        257 HP-PLSLGSITSPKRGGNN----NGHEPSDIIMPLRPSEAG--AFCPHYEKVSGDYGHPV 309

Qy        323 YIVQDGPPQSPPNIYY 338
              |||||   ||| ||||
Db        310 YIVQDMASQSPANIYY 325


RESULT 3
Q9PUJ4
ID   Q9PUJ4      PRELIMINARY;      PRT;   333 AA.
AC   Q9PUJ4;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Ephrin-B2 precursor.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Menzel P., Pasquale E.B.;
RT   "Coding sequence of chicken ephrin-B2.";
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF180729; AAD53948.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008972; Cupredoxin.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Signal.
FT   SIGNAL        1     27       POTENTIAL.
FT   CHAIN        28    333       EPHRIN-B2.
SQ   SEQUENCE   333 AA;  36761 MW;  4C28E8CB211B7783 CRC64;

  Query Match             25.3%;  Score 620.5;  DB 13;  Length 333;
  Best Local Similarity   40.2%;  Pred. No. 2.8e-41;
  Matches  133;  Conservative   52;  Mismatches  125;  Indels   21;  Gaps    6;

Qy         14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
              |||::|    |   : |:|:||||:| :|    | ||||||||:||::||:       :
Db         16 GALMVLWRTALAKSIVLDPIYWNSSNPKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 72

Qy         74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
               ||:|||:|:|   |   |         || | :|| |::|||||||:|||||| ||: :
Db         73 GQYEYYKVYMVDKDQADSCAIRKDNTPLLNCAKPDQDVKFTIKFQEFSPNLWGLEFQKNK 132

Qy        134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMER----- 188
              |||:|:||:|: ||| : :|||| |: ||:|::||| |    :||   |  | :|
Db        133 DYYVISTSNGSLEGLNNQEGGVCQTKTMKILMKVGQDPNSAGLPR---STDPTKRPEQEA 189

Qy        189 -DRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGG 247
                 | : :  |  ::  |  |    |:     :    :   || | |  : :: :
```

```
Db        190 GTNGKSSTTSPFVKDHSGSSTDG--SKAGHSSILGSEVALFAGIASGCIIFIVIIITLVV 247

Qy        248 AMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPF 307
              :   ||| :    :|    |     :    |        :|| :: | ||    ||  |
Db        248 LLLKYRRRHRKHSPQHTTTLSLSTLATPKRSGNN----NGSEPSDIIIPLR---TADSVF 300

Qy        308 CPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
              ||||||||||||||||||: ||||| ||||
Db        301 CPHYEKVSGDYGHPVYIVQEMPPQSPANIYY 331


RESULT 4
Q90Z33
ID   Q90Z33      PRELIMINARY;      PRT;   341 AA.
AC   Q90Z33;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Ephrin B1.
GN   EFNB1.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21290827; PubMed=11397014;
RA   Chan J., Mably J.D., Serluca F.C., Chen J.N., Goldstein N.B.,
RA   Thomas M.C., Cleary J.A., Brennan C., Fishman M.C., Roberts T.M.;
RT   "Morphogenesis of prechordal plate and notochord requires intact
RT   eph/ephrin b signaling.";
RL   Dev. Biol. 234:470-482(2001).
DR   EMBL; AF375224; AAK64274.1; -.
DR   ZFIN; ZDB-GENE-010618-2; efnb1.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008972; Cupredoxin.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
SQ   SEQUENCE   341 AA;  37849 MW;  CB922F20E0D93E94 CRC64;

  Query Match             24.8%;  Score 607;  DB 13;  Length 341;
  Best Local Similarity   41.5%;  Pred. No. 3.5e-40;
  Matches  139;  Conservative   49;  Mismatches  109;  Indels   38;  Gaps   11;

Qy         24 LVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYL 83
              | :  ||| | ||| | :| :  | |:||:|||:||::||:    |    | ||||||||
Db         23 LPAAKSLESVVWNSQNPKFVSGKGLVIYPEIGDKLDIICPK----GDMGRP-YEFYKLYL 77

Qy         84 VGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDG 143
              |   |   |     ||:|:||::|: |::|||||||:|||  | ||:   :||| :||:|
Db         78 VKKEQAESCSTILDPNVLVTCNKPEKDIKFTIKFQEFSPNYMGLEFKRFTNYYITSTSNG 137

Qy        144 TREGLESLQGGVCLTRGMKVLLRVGQSPRG-----GAVPRKPVSEMPMERDRGAAHSLEP 198
```

```
              |:|||||: :|||| || ||:::::||| |          :| :|      :     :   |
Db        138 TQEGLENREGGVCSTRSMKIIMKVGQDPNAPDPDLPDLPDRPYDNEIKDPTTSPSRKTER 197

Qy        199 GKEN--------LPGDPTSNATSR--GAEGPLPPPSMPAVAGAAG-GLALLLLGVAGAGG 247
              |:||        :||  | |  :     ||     | ||:  | | |  : || :
Db        198 GRENEVDGNGSKMPGKDTRNQNNSPGSVEGIF--GSKPALFAAIGAGCVIFLLIIIILIV 255

Qy        248 AMCWRRRRAKPSESRHPGPGSFGRGGSL----GLGGGGGMGPREAEPGELGIALRGGGAA 303
               :   |:| :    :|  |    |||:      |    |     :|| :: | ||
Db        256 LLLKLRKRTR----KHSQP----RGGTALSLSTLATPKGAAQAGSEPSDIIIPLR---TT 304

Qy        304 DPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
              :  :||||||||||||||||||: ||||| ||||
Db        305 ENNYCPHYEKVSGDYGHPVYIVQEMPPQSPANIYY 339


RESULT 5
Q90Z32
ID   Q90Z32      PRELIMINARY;      PRT;   334 AA.
AC   Q90Z32;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Ephrin B2b.
GN   EFNB2B.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21290827; PubMed=11397014;
RA   Chan J., Mably J.D., Serluca F.C., Chen J.N., Goldstein N.B.,
RA   Thomas M.C., Cleary J.A., Brennan C., Fishman M.C., Roberts T.M.;
RT   "Morphogenesis of prechordal plate and notochord requires intact
RT   eph/ephrin b signaling.";
RL   Dev. Biol. 234:470-482(2001).
DR   EMBL; AF375226; AAK64276.1; -.
DR   ZFIN; ZDB-GENE-010618-1; efnb2b.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008972; Cupredoxin.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
SQ   SEQUENCE   334 AA;  36998 MW;  341497E0FE9473BD CRC64;

  Query Match             24.3%;  Score 596.5;  DB 13;  Length 334;
  Best Local Similarity   40.6%;  Pred. No. 2.3e-39;
  Matches  132;  Conservative   45;  Mismatches  113;  Indels   35;  Gaps    8;

Qy         30 LEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQG 89
              || :|||::| :|    | |||||||||::|::||| : ||     | |::::|||   |
Db         27 LESIYWNTSNTKFVPGRGVVLYPQIGDKMDIVCPRIK-PGSTEQTNIEYFRVYLVPKEQL 85

Qy         90 RRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGTREGLE 149
```

```
                |    :  ||| ||:|| |::|| |||||:|||||| ||    ||:||:||: | |||:
Db         86 ETCHVTKSDMLLLNCDKPDQDVKFTFKFQEFSPNLWGLEFLRGKDYHIISTSNSTFEGLD 145

Qy        150 SLQGGVCLTRGMKVLLRVGQSPRGGAV----PRKPVSEMPMERDRGAAHSLEPGKENLPG 205
              :  |||| :: ||::|||||||         | :   : |  :|:         |||
Db        146 NHHGGVCRSKSMKLVLRVGQSPTDSFSAKNHPTRNPPKYPENKDQNTF-----SKENDVS 200

Qy        206 --DPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMCW---------RR 253
                |   |  | |  |           |:||    |  ||  | ||: :
Db        201 QIDSMQNGESGGKSG--------ESVGSAGSDVALFAGV--ASGAVIFILIIIALVALLH 250

Qy        254 RRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEK 313
              || :   ::  |          | |  ||     :|| ::   :|  |:    :||||||
Db        251 RRHQKHSAQCSGQLPLNTLPKRGSGASGGSNNNGSEPSDIIFPIRTSGSM---YCPHYEK 307

Qy        314 VSGDYGHPVYIVQDGPPQSPPNIYY 338
              |||||||||||||: |||:| ||||
Db        308 VSGDYGHPVYIVQEMPPQNPANIYY 332
```

```
RESULT 6
Q9W6H9
ID   Q9W6H9      PRELIMINARY;      PRT;   205 AA.
AC   Q9W6H9;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Ephrin-B2 (Fragment).
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97411149; PubMed=9259557;
RA   Smith A., Robinson V., Patel K., Wilkinson D.G.;
RT   "The EphA4 and EphB1 receptor tyrosine kinases and ephrin-B2 ligand
RT   regulate targeted migration of branchial neural crest cells.";
RL   Curr. Biol. 7:561-570(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20099673;
RA   Helbling P.M., Saulnier D.M., Robinson V., Christiansen J.H.,
RA   Wilkinson D.G., Brandli A.W.;
RT   "Comparative analysis of embryonic gene expression defines potential
RT   interaction sites for Xenopus EphB4 receptors with ephrin-B ligands.";
RL   Dev. Dyn. 216:361-373(1999).
DR   EMBL; AF128844; AAD32610.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008972; Cupredoxin.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   ProDom; PD002533; Ephrin; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   205 AA;  22256 MW;  7DEDD34277260C87 CRC64;
```

```
  Query Match             13.5%;  Score 331;  DB 13;  Length 205;
  Best Local Similarity   36.4%;  Pred. No. 1.7e-18;
  Matches   82;  Conservative   35;  Mismatches   72;  Indels   36;  Gaps    7;

Qy        128 EFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSP-----RGGAVPRKPVS 182
              ||:   |||||:||:|: ||::: :||||:|: ||:|::||| |     || :  |:|
Db          1 EFQRDKDYYIISTSNGSLEGVDNQEGGVCVTKAMKILMKVGQDPNFHNHRGASSTRRPDH 60

Qy        183 EMPM--ERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
              |     :    : |   |   :  |    :::  |:|  |        || | |  : ::
Db         61 ESGTNGKSSTTSPHVNGPEGSSTEGKNAGHSSILGSEVAL-------FAGIASGSIIFIV 113

Qy        241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLG-------GGGGMGPREAEPGEL 293
               :      :   ||| :    :|          :| |         |   |   :|| ::
Db        114 IIITLVVLLLKYRRRHRKHSPQHT---------TLSLSTLATPKRSGNNNG---SEPSDI 161

Qy        294 GIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
               | ||    |:  |||||||||||||||||||: ||||| ||||
Db        162 IIPLR---TAEGVFCPHYEKVSGDYGHPVYIVQEMPPQSPANIYY 203


RESULT 7
Q9U3M2
ID   Q9U3M2      PRELIMINARY;      PRT;   237 AA.
AC   Q9U3M2;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   C43F9.8 protein.
GN   C43F9.8.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Mortimore B.J.;
RL   Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99069613; PubMed=9851916;
RA   none;
RT   "Genome sequence of the nematode C.elegans: A platform for
RT   investigating biology.";
RL   Science 282:2012-2018(1998).
DR   EMBL; Z82262; CAB54195.1; -.
DR   PIR; T19914; T19914.
DR   WormPep; C43F9.8; CE23593.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008972; Cupredoxin.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
SQ   SEQUENCE   237 AA;  26748 MW;  B9B2D9FCC71FE4FC CRC64;

  Query Match             8.8%;  Score 214.5;  DB 5;  Length 237;
```

```
  Best Local Similarity   25.7%;  Pred. No. 3.7e-09;
  Matches   53;  Conservative   41;  Mismatches   83;  Indels   29;  Gaps    6;

Qy          11 VRVGALLLLGVLGLVS-GLSLEPVYWNSANKRFQAEG-GYVLYPQIGDRLDLLCPRARPP 68
               :::   :|| :   :     :  : | |:|  |      :|:   ||||: : ||::
Db           1 MQIATFILLSLFPFIGWARKIPDINWISSNPIFDVSNTDHVISVHIGDRVSIRCPKSDET 60

Qy          69 GPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHE 128
               |      ||:  :|:|   :   |     | |:  ||   ::    | |: ::|   | |
Db          61 G-----KYEYSYIYMVSDEEYDHCFL-SKPRLVGACDNQTINASINIVFRSFTPTPGGFE 114

Qy         129 FRSHHDYYIIA------------------TSDGTREGLESLQGGVCLTRGMKVLLRVGQ 169
               |:   :|::|:                  |||||  ||::  : |:|  : ||:   |||
Db         115 FQPGKNYFLISKSEVDALIIYETANQIFPGTSDGTLEGIDRKKDGLCTAKQMKIKFEVGQ 174

Qy         170 SPRGGAVPRKPVSEMPMERDRGAAHS 195
                 ||   |:   :   :::|| | ||
Db         175 DRRGIENPK--FAARTLKKDRDAEHS 198


RESULT 8
Q9U474
ID   Q9U474      PRELIMINARY;      PRT;   279 AA.
AC   Q9U474;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   VAB-2 (Hypothetical protein Y37E11AR.6).
GN   VAB-2 OR Y37E11AR.6.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=N2;
RX   MEDLINE=20084449; PubMed=10619431;
RA   Chin-Sang I.D., George S.E., Ding M., Moseley S.L., Lynch A.S.,
RA   Chisholm A.D.;
RT   "The ephrin VAB-2/EFN-1 functions in neuronal signaling to regulate
RT   epidermal morphogenesis in C. elegans.";
RL   Cell 99:781-790(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RX   MEDLINE=99069613; PubMed=9851916;
RA   None;
RT   "Genome sequence of the nematode C. elegans: a platform for
RT   investigating biology. The C. elegans Sequencing Consortium.";
RL   Science 282:2012-2018(1998).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Miller N., Maggi L.;
RT   "The sequence of C. elegans cosmid Y37E11AR.";
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [4]
```

```
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Waterston R.;
RT   "Direct Submission.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF201079; AAF25647.1; -.
DR   EMBL; AC024759; AAK68436.1; -.
DR   WormPep; Y37E11AR.6; CE27606.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008972; Cupredoxin.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
SQ   SEQUENCE   279 AA;  32068 MW;  8C291A92D97D39EF CRC64;

  Query Match             8.1%;  Score 198.5;  DB 5;  Length 279;
  Best Local Similarity   27.8%;  Pred. No. 8.4e-08;
  Matches   64;  Conservative   35;  Mismatches   90;  Indels   41;  Gaps    8;

Qy          1 MGPPHSGPGGVRVGALLLLGVLGLV--SGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRL 58
              | ||      :::  :||  :|  |  |   |  :|||| |   :       |  ||| |
Db          1 MHPP------IKIQTILLF-ILTTVHCSAKRLPQIYWNSTNPLVER------YAAIGDTL 47

Qy         59 DLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQ 118
             |::||       :|    |   :| |   :   ||       |  | :|  : :  : |:
Db         48 DIVCPFF---DENSDELTEQSIIYRVTEEEYENCERRSKAKELGRCTQPYQEEKLKVAFR 104

Qy        119 EYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPR 178
               |||  | ::|    || |:|| |:|:|| : |||:|  :  :|::: :  : | |
Db        105 LMSPNPSGLDYRPGVTYYFISTSTGSRKGLYNEQGGLCASHNLKMVIHI--TDRNG---- 158

Qy        179 KPVSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAV 228
                    | |  |     |:      || :||        | ::| |
Db        159 ----------DIGPHHHRHHHKKTTTTTTTSTSTS-------TPKTIPPV 191


RESULT 9
Q9V4E1
ID   Q9V4E1      PRELIMINARY;      PRT;   652 AA.
AC   Q9V4E1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Ephrin protein (LD11109p).
GN   EPHRIN OR CG1862 OR DSIM\EPHRIN;EPHRIN.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Dai Y., Kunes S.;
RT   "Isolation and Characterization of Drosophila Ephrin.";
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
```

RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF216287; AAF28394.1; -.
DR EMBL; AE003843; AAF59335.2; -.
DR EMBL; BT005199; AAO61756.1; -.
DR FlyBase; FBgn0040324; Ephrin.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008972; Cupredoxin.

```
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
SQ   SEQUENCE   652 AA;  72302 MW;  5BA2F02F15964594 CRC64;

  Query Match             7.8%;  Score 192;  DB 5;  Length 652;
  Best Local Similarity   21.2%;  Pred. No. 7.7e-07;
  Matches  103;  Conservative   64;  Mismatches  154;  Indels  164;  Gaps   22;

Qy         33 VYWNSANKRFQAEG-GYVLYPQIG------DRLDLLCPRARPPGPHSSPNYEFYKLYLVG 85
              ::||::|  |: :   :::    |      |:: ::||    ||   :   | | :| |
Db        219 MHWNTSNSIFRIDNTDHIIDVNKGNLAFEFDQVHIICP-VYEPGTFENET-EKYIIYNVS 276

Qy         86 GAQGRRCEAPPA-PNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGT 144
                :   |    | | ::  ||:|   : ||| |: ::|   | ||   :||| |:||  :
Db        277 KVEYETCRITNADPRVIAICDKPQKLMFFTITFRPFTPQPGGLEFLPGNDYYFISTS--S 334

Qy        145 REGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSL-----EPG 199
              :: |    || | |  |||: :|  :|         :|      | | | ::     :
Db        335 KDDLYRRIGGRCSTNNMKVVFKVCCAPEDNN-KTTALSNSKSVTDTGGAINVNIANNDES 393

Qy        200 KENLPGDPTSNATSRGAEG-----------PLPP-----------------------P 223
                |  |:  :  |: |  |            |: |                       |
Db        394 HVNSHGNNIAIGTNIGINGGQIIGGPQSAGIPINPLSGNNNINGIPTTINSNIDQFNRIP 453

Qy        224 SMPAVAGAAGGLALLLLGVAGAGGAMCWRRRRAKPSESRHPGPG-SFGRGGSLGLGGGGG 282
                | : |   |   :  |: | || :               || : |    |  | ||
Db        454 IQPNIIGNHVGTNAVGTGIVGGGGIIL-------------TPGHAHGNINMLQPGRGGI 499

Qy        283 MGPREAEPG----ELGIALRG-----------------GGAADPPFCPHYEKVSGDYGH 320
                |   | ||    : || :                    |  |     || |      |
Db        500 NG---AYPGHHHIQTGIRINNVPTQHNYPSHKGNANSNINGNDDH---HHYNK------H 547

Qy        321 PVYIVQD-------GPPQSPPNIYYTSISVLEWPILHTIQLFFMRSKCSRVTTFLFPVQV 373
              |  :|::       |   |  ||:   | :|                       :||  :
Db        548 PNEVVKNEELTYNSGAATSDGNIFALWIWILS----------------------IFP--L 583

Qy        374 ITTSTCRMTSFSFTTLNPSMQACRAQMGEFRIRWCFWGDRILGTALFVLVLILLLGRLNM 433
              ::  :| ::|:                      |         :| |::  | :||   :
Db        584 LSIQSCHLSSY--------------------WI--------SASFLVSTIAILGIHYL 613

Qy        434 HQTTL 438
                | ||
Db        614 IQITL 618


RESULT 10
Q98TZ1
ID   Q98TZ1      PRELIMINARY;      PRT;   202 AA.
AC   Q98TZ1;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Ephrin-A6 (Fragment).
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Menzel P., Valencia F., Godement P., Dodelet V.C., Pasquale E.B.;
RT   "Ephrin-A6, a new ligand for EphA receptors in the developing visual
RT   system.";
RL   Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF317286; AAK00944.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008972; Cupredoxin.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   202 AA;  22624 MW;  91E2716FF91353F9 CRC64;

  Query Match             7.3%;  Score 178.5;  DB 13;  Length 202;
  Best Local Similarity   27.5%;  Pred. No. 2.2e-06;
  Matches   56;  Conservative   27;  Mismatches   84;  Indels   37;  Gaps    7;

Qy         33 VYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRC 92
              |||| :| ||  :  | :   | | ||: ||    | | :    | : |::|     | |
Db         25 VYWNGSNPRF-LQDDYSIQVSINDHLDIYCPHYSAPTPWA----ESFTLFMVDEEGYRGC 79

Qy         93 EAPPAPNLLLTCDR---PDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIAT-SDGTREGL 148
                 |       |::   | : :||: | | ::|   | |||    || |:  : |:
Db         80 SETPGAFKRWECNKPFAPFVPVRFSEKIQRFTPFSLGFEFRPGETYYYISVPTPGS---- 135

Qy        149 ESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLPGDPT 208
                | ||   : |  |        |   :|::|:|  : ||             | |
Db        136 ----AGRCLKLRVSVCCR--------ASTPEPLTEVPNSQPRGR----------GGPE 171

Qy        209 SNATSRGAEGPLPPPSMPAVAGAA 232
               :| |     |:|  |   :   |
Db        172 GDAGSPRDAAPIPQRSRTRLVALA 195


RESULT 11
Q8N578
ID   Q8N578      PRELIMINARY;      PRT;   205 AA.
AC   Q8N578;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Ephrin-A1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Strausberg R.;
```

```
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC032698; AAH32698.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008972; Cupredoxin.
DR   InterPro; IPR001799; Ephrin.
DR   InterPro; IPR001680; WD40.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
DR   PROSITE; PS00678; WD_REPEATS_1; 1.
SQ   SEQUENCE   205 AA;  23785 MW;  4FE9A6D94C1251A9 CRC64;

  Query Match             6.9%;  Score 168.5;  DB 4;  Length 205;
  Best Local Similarity   27.5%;  Pred. No. 1.4e-05;
  Matches   52;  Conservative   33;  Mismatches   85;  Indels   19;  Gaps    7;

Qy         18 LLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPN-- 75
              |||:   ::      |:||||:| :|: |  | :: |: | :|::||       ||  :
Db          8 LLGLCCSLAAADRHTVFWNSSNPKFRNE-DYTIHVQLNDYVDIICPHYE---DHSVADAA 63

Qy         76 YEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSH 132
               | | ||||   : : |:      :   |:||       : : ||| ::|   | ||:
Db         64 MEQYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKEFKEG 123

Qy        133 HDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVP--RKPVSEMPMERD- 189
              | || |:      |         ||   : |  ::  ||:    |  ::  :: |  |
Db        124 HSYYYISKPIHQHEDR-------CLRLKVTVSGKITHSPQAHVNPQEKRLAADDPEVRVL 176

Qy        190 RGAAHSLEP 198
                 |||  |
Db        177 HSIAHSAAP 185


RESULT 12
Q9D7K8
ID   Q9D7K8      PRELIMINARY;      PRT;   205 AA.
AC   Q9D7K8;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Adult male tongue cDNA, RIKEN full-length enriched library,
DE   clone:2310004J15, full insert sequence.
GN   EFNA1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Tongue;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
```

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK009144; BAB26102.1; -.
DR MGD; MGI:103236; Efna1.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008972; Cupredoxin.
DR InterPro; IPR001799; Ephrin.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00812; Ephrin; 1.
DR PRINTS; PR01347; EPHRIN.
DR ProDom; PD002533; Ephrin; 1.
DR PROSITE; PS01299; EPHRIN; 1.
DR PROSITE; PS00678; WD_REPEATS_1; 1.
SQ SEQUENCE 205 AA; 23772 MW; E37E55767459A4EC CRC64;

Query Match 6.8%; Score 167; DB 11; Length 205;
Best Local Similarity 26.1%; Pred. No. 1.9e-05;
Matches 43; Conservative 34; Mismatches 76; Indels 12; Gaps 4;

```
Qy         18 LLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYE 77
              |||:   ::      |:|||:| :|: |  | :: |: | ||::||        :    |
Db          8 LLGLCCSLAAADRHIVFWNSSNPKFREE-DYTVHVQLNDYLDIICPHYEDDSV-ADAAME 65

Qy         78 FYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHHD 134
               | ||:|   :   |:      :   |:||       : ::||| ::| : | ||:  |
Db         66 RYTLYMVEHQEYVACQPQSKDQVRWNCNRPSAKHGPEKLSVKFQRFTPFILGKEFKEGHS 125

Qy        135 YYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRK 179
              || |:     :|         ||   : |  ::  :|:    |::
Db        126 YYYISKPIYHQE-------SQCLKLKVTVNGKITHNPQAHVNPQE 163
```

RESULT 13
Q9CZS8
ID Q9CZS8 PRELIMINARY; PRT; 206 AA.
AC Q9CZS8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 10 days embryo cDNA, RIKEN full-length enriched library,
DE clone:2610529M21, full insert sequence.
GN EFNA4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Embryo;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK012195; BAB28092.1; -.
DR   MGD; MGI:106643; Efna4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008972; Cupredoxin.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
SQ   SEQUENCE   206 AA;  22859 MW;  675E32971D1C6EBC CRC64;

  Query Match             6.7%;  Score 163.5;  DB 11;  Length 206;
  Best Local Similarity   28.1%;  Pred. No. 3.6e-05;
  Matches   61;  Conservative   17;  Mismatches   80;  Indels   59;  Gaps   10;

Qy         32 PVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRR 91
              |:||||:| |    |  |:     | ||: ||    |||   |  | : ||:|  :
Db         29 PIYWNSSNPRL-LRGDAVVELGFNDYLDIFCPHYESPGPPEGP--ETFALYIVDWSGYEA 85

Qy         92 CEAPPAPNL-LLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGTREG 147
              | |  | :    |  |      :||: | | |:|   | ||     || |:       |
Db         86 CTAEGANSFQRWNCSMPFAPFSPVRFSEKIQRYTPFPLGFEFLPGETYYYISVPTPESPG 145

Qy        148 -LESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAH-SLEPGKENLPG 205
                 ||  ||                                  :: |::| |  |      |
Db        146 RCLRLQVSVCC-----------------------------KESGSSHESAHP-----VG 170

Qy        206 DPTSNATS--RGAEGPLPPPSMPAVAGAAGGLALLLL 240
               |  : ||  ||   | |             | ||||
Db        171 SPGESGTSGWRGGHAPSP-------------LCLLLL 194
```

```
RESULT 14
Q9N178
ID   Q9N178      PRELIMINARY;      PRT;   675 AA.
AC   Q9N178;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Type X collagen.
GN   COL10A1.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21015405; PubMed=11130976;
RA   Nielsen V.H., Bendixen C., Arnbjerg J., Sorensen C.M., Jensen H.E.,
RA   Shukri N.M., Thomsen B.;
RT   "Abnormal growth plate function in pigs carrying a dominant mutation
RT   in type X collagen.";
RL   Mamm. Genome 11:1087-1092(2000).
DR   EMBL; AF222861; AAF37271.1; -.
DR   InterPro; IPR001073; C1q.
DR   InterPro; IPR008161; C1g_helix.
DR   InterPro; IPR008160; Collagen.
DR   InterPro; IPR008983; TNF_like.
DR   Pfam; PF00386; C1q; 1.
DR   Pfam; PF01391; Collagen; 8.
DR   PRINTS; PR00007; COMPLEMNTC1Q.
DR   ProDom; PD000007; C1g_helix; 2.
DR   SMART; SM00110; C1Q; 1.
DR   PROSITE; PS01113; C1Q; 1.
KW   Collagen.
SQ   SEQUENCE   675 AA;  65447 MW;  26397B10310383F9 CRC64;

  Query Match             6.3%;  Score 155.5;  DB 6;  Length 675;
  Best Local Similarity   28.5%;  Pred. No. 0.00064;
  Matches  103;  Conservative   17;  Mismatches  113;  Indels  129;  Gaps   25;

Qy          1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQI-GDR-L 58
              ||||  || ||                                ||   | |:   | | |||
Db        212 MGPP--GPPGV--------------------------GKR--GENGFPGQPGIKGDRGF 240

Qy         59 DLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRR-CEAPPAPNLLLTCDRPDLDLRFTIKF 117
                 | ||||   |           | |||     | ||       :| |
Db        241 PGESGPAGPPGPQGPP----------GEQGREGIGKPGAPG---AAGQPGL-------- 278

Qy        118 QEYSPNLWGHEFRSHHDYYIIATSDGT----REGLESLQGGVCLTRGMKVLLRVGQSPRG 173
                  |   ||          :|   |     : ||  |:|     ||          | |
Db        279 ----PGTKGHPGAPG-----MAGPPGAPGFGKPGLPGLKG----QRG----------PIG 315

Qy        174 GAVPRKPVSEMPMERDRG-AAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAA 232
                :|  | :    : ::| | |  |||    ||       ||| :||   |    | |
Db        316 --LPGAPGA----KGEQGPAGHPGEPGLTGPPG-------SRGPQGPKGIPGNNGVPGPK 362

Qy        233 GGLALLLLGVAGAGGAMCWRRRR---AKPSESRHPG-------PGSFGRGGSLGLGGGGG 282
```

```
                | :   | | ||  ||   |       ||     ||       ||  |  |  |:||  |
Db        363 GEIG--LAGPAGFPGAKGERGPSGLDGKPGYPGEPGLNGPKGNPGLPGPKGDPGIGGPPG 420

Qy        283 M----GPREAE--PGELGIA-LRGG-------GAADPPFCPHYEKVSGDYGHPVYIVQDG 328
              :    ||  |:  ||  | |  ||        |   ||  | :    || |:|      |
Db        421 LPGPVGPAGAKGVPGHNGEAGPRGAPGIPGTRGPIGPPGIPGFPGSKGDPGNP------G 474

Qy        329 PP 330
              ||
Db        475 PP 476
```

RESULT 15
O93431
ID   O93431   PRELIMINARY;   PRT;   229 AA.
AC   O93431;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Ephrin A-L1.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Durbin L., Brennan C.H., Shiomi K., Cooke J.;
RT   "Eph signalling is required for segmentation and differentiation of
RT   the somites.";
RL   Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ006838; CAA07264.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008972; Cupredoxin.
DR   InterPro; IPR001799; Ephrin.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
DR   PROSITE; PS00290; IG_MHC; 1.
SQ   SEQUENCE   229 AA; 26115 MW; 8684462F67AF6F5C CRC64;

  Query Match   6.3%; Score 155; DB 13; Length 229;
  Best Local Similarity   27.2%; Pred. No. 0.00019;
  Matches   56; Conservative   23; Mismatches   93; Indels   34; Gaps   7;

```
Qy         33 VYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRC 92
              ||||| |  |  :  | :  :| | ||::||     |  :|   | | ||:|       |
Db         25 VYWNSTNANFLWD-DYTVDVRINDYLDIICPH-YAHGEIASQEAERYVLYMVELEDYENC 82

Qy         93 EAPPAPNLLLTCDR---PDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGTREGLE 149
              :      |   | |   |    :|: ||| ::|   | |||    || |:         :
Db         83 KPHSFDQLRWECSRPFAPHAPEKFSEKFQRFTPFTLGKEFRQGESYYYIS---------K 133

Qy        150 SL--QGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLPGDP 207
               |   |  ||   : |:      | |    :| | ::     : ||  :      || |
```

```
Db        134 PLHHHGQECLRLKVDVV-----GPHGSKNKKKMVEKVEEIEGKMAAGGVHNPSNRLPADD 188

Qy        208 TSNATSRGAEGPLPPPSMPAVAGAAG 233
                          |   :| |  : |
Db        189 -------------PIAMIPVVQRSVG 201
```

Search completed: April 13, 2004, 09:28:08
Job time : 69.9623 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 13, 2004, 09:22:17 ; Search time 24.0377 Seconds
(without alignments)
985.614 Million cell updates/sec

Title: US-10-021-121-2
Perfect score: 2450
Sequence: 1 MGPPHSGPGGVRVGALLLLG.....TTLLRQRASVEAEAGQHGPL 455

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1841	75.1	340	1	EFB3_HUMAN	Q15768 homo sapien
2	1771	72.3	340	1	EFB3_MOUSE	O35393 mus musculu
3	628.5	25.7	336	1	EFB2_MOUSE	P52800 mus musculu
4	623	25.4	346	1	EFB1_HUMAN	P98172 homo sapien
5	620.5	25.3	333	1	EFB2_HUMAN	P52799 homo sapien
6	619	25.3	334	1	EFB1_CHICK	O73612 gallus gall
7	617.5	25.2	332	1	EFB2_BRARE	O73874 brachydanio
8	604.5	24.7	345	1	EFB1_MOUSE	P52795 mus musculu
9	599.5	24.5	345	1	EFB1_RAT	P52796 rattus norv
10	591	24.1	327	1	EFB1_XENLA	O13097 xenopus lae
11	185	7.6	195	1	EFA2_BRARE	P79727 brachydanio
12	179	7.3	238	1	EFA3_HUMAN	P52797 homo sapien
13	176	7.2	209	1	EFA2_MOUSE	P52801 mus musculu
14	175.5	7.2	213	1	EFA2_HUMAN	O43921 homo sapien
15	172	7.0	200	1	EFA2_CHICK	P52802 gallus gall
16	170.5	7.0	228	1	EFA5_CHICK	P52804 gallus gall
17	169.5	6.9	201	1	EFA4_HUMAN	P52798 homo sapien

18	169.5	6.9	228	1	EFA5_BRARE	P79728	brachydanio
19	167.5	6.8	216	1	EFA1_XENLA	P52794	xenopus lae
20	167.5	6.8	228	1	EFA5_HUMAN	P52803	homo sapien
21	167.5	6.8	228	1	EFA5_MOUSE	O08543	mus musculu
22	167.5	6.8	228	1	EFA5_RAT	P97605	rattus norv
23	166	6.8	205	1	EFA1_HUMAN	P20827	homo sapien
24	162.5	6.6	205	1	EFA1_RAT	P97553	rattus norv
25	161	6.6	205	1	EFA1_MOUSE	P52793	mus musculu
26	160.5	6.6	206	1	EFA4_MOUSE	O08542	mus musculu
27	159	6.5	680	1	CA1A_MOUSE	Q05306	mus musculu
28	154.5	6.3	1049	1	CA13_BOVIN	P04258	bos taurus
29	151.5	6.2	301	1	CC02_CAEEL	P17656	caenorhabdi
30	148.5	6.1	1670	1	CA34_HUMAN	Q01955	homo sapien
31	146.5	6.0	1774	1	CA1H_MOUSE	P39061	mus musculu
32	146	6.0	1027	1	CAFF_RIFPA	P30754	riftia pach
33	145	5.9	674	1	CA1A_BOVIN	P23206	bos taurus
34	145	5.9	1745	1	CA35_HUMAN	P25940	homo sapien
35	144.5	5.9	1516	1	CA1H_HUMAN	P39060	homo sapien
36	144	5.9	675	1	CA39_CHICK	P32017	gallus gall
37	144	5.9	921	1	CA19_HUMAN	P20849	homo sapien
38	143	5.8	674	1	CA1A_CHICK	P08125	gallus gall
39	142.5	5.8	635	1	CA28_HUMAN	P25067	homo sapien
40	142.5	5.8	1496	1	CA25_HUMAN	P05997	homo sapien
41	142	5.8	744	1	CA18_HUMAN	P27658	homo sapien
42	142	5.8	1029	1	CA26_MOUSE	Q02788	mus musculu
43	142	5.8	1763	1	CA24_ASCSU	P27393	ascaris suu
44	141.5	5.8	1466	1	CA13_HUMAN	P02461	homo sapien
45	141	5.8	744	1	CA18_RABIT	P14282	oryctolagus

ALIGNMENTS

```
RESULT 1
EFB3_HUMAN
ID   EFB3_HUMAN     STANDARD;      PRT;   340 AA.
AC   Q15768; O00680; Q8TBH7; Q92875;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Ephrin-B3 precursor (EPH-related receptor tyrosine kinase ligand 8)
DE   (LERK-8) (EPH-related receptor transmembrane ligand ELK-L3).
GN   EFNB3 OR EPLG8 OR LERK8.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Cerretti D.P.;
RL   Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=97271551; PubMed=9126477;
RA   Tang X.X., Pleasure D.E., Ikegaki N.;
RT   "cDNA cloning, chromosomal localization, and expression pattern of
```

RT EPLG8, a new member of the EPLG gene family encoding ligands of EPH-
RT related protein-tyrosine kinase receptors.";
RL Genomics 41:17-24(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain cortex;
RX MEDLINE=96404527; PubMed=8808709;
RA Gale N.W., Flenniken A., Compton D.C., Jenkins N.A., Copeland N.G.,
RA Gilbert D.J., Davis S., Wilkinson D.G., Yancopoulos G.D.;
RT "Elk-L3, a novel transmembrane ligand for the Eph family of receptor
RT tyrosine kinases, expressed in embryonic floor plate, roof plate and
RT hindbrain segments.";
RL Oncogene 13:1343-1352(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: May play a pivotal role in forebrain function. Binds to,
CC and induce the collapse of, commissural axons/growth cones in
CC vitro. May play a role in constraining the orientation of
CC longitudinally projecting axons (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Highly expressed in brain; expressed in
CC embryonic floor plate, roof plate and hindbrain segments.
CC -!- SIMILARITY: Belongs to the ephrin family.
CC --
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC --
DR EMBL; U57001; AAB05170.1; -.
DR EMBL; U66406; AAC51203.1; -.
DR EMBL; U62775; AAC50707.1; -.

```
DR   EMBL; BC022499; AAH22499.1; -.
DR   EMBL; BC042944; AAH42944.1; -.
DR   Genew; HGNC:3228; EFNB3.
DR   MIM; 602297; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0005005; F:transmembrane-ephrin receptor activity; TAS.
DR   GO; GO:0007267; P:cell-cell signaling; TAS.
DR   GO; GO:0007399; P:neurogenesis; TAS.
DR   InterPro; IPR008972; Cupredoxin.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;
KW   Signal; Polymorphism.
FT   SIGNAL        1     27       POTENTIAL.
FT   CHAIN        28    340       EPHRIN-B3.
FT   DOMAIN       28    226       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    227    247       POTENTIAL.
FT   DOMAIN      248    340       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      338    340       PDZ RECOGNITION MOTIF (POTENTIAL).
FT   DISULFID     62    104       BY SIMILARITY.
FT   DISULFID     92    156       BY SIMILARITY.
FT   CARBOHYD    210    210       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT     166    166       R -> Q.
FT                                /FTId=VAR_002356.
SQ   SEQUENCE   340 AA;  35834 MW;  EDFF2A23C2FDE79F CRC64;
```

Query Match 75.1%; Score 1841; DB 1; Length 340;
Best Local Similarity 100.0%; Pred. No. 1e-113;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

Qy         61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy        121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180

Qy        181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

Qy        241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGGMGPREAEPGELGIALRGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGGMGPREAEPGELGIALRGG 300

Qy        301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
              ||||||||||||||||||||||||||||||||||||||
Db        301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
```

```
RESULT 2
EFB3_MOUSE
ID   EFB3_MOUSE     STANDARD;      PRT;   340 AA.
AC   O35393;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Ephrin-B3 precursor.
GN   EFNB3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=98143367; PubMed=9484836;
RA   Bergemann A.D., Zhang L., Chiang M.-K., Brambilla R., Klein R.,
RA   Flanagan J.G.;
RT   "Ephrin-B3, a ligand for the receptor EphB3, expressed at the midline
RT   of the developing neural tube.";
RL   Oncogene 16:471-480(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   FUNCTION.
RX   MEDLINE=20171264; PubMed=10704386;
RA   Imondi R., Wideman C., Kaprielian Z.;
RT   "Complementary expression of transmembrane ephrins and their receptors
RT   in the mouse spinal cord: a possible role in constraining the
RT   orientation of longitudinally projecting axons.";
RL   Development 127:1397-1410(2000).
CC   -!- FUNCTION: May play a pivotal role in forebrain function. Binds to,
CC       and induce the collapse of, commissural axons/growth cones in
```

```
CC       vitro. May play a role in constraining the orientation of
CC       longitudinally projecting axons.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: Expressed on lateral floor plate cells,
CC       specifically on commissural axon segments that have passed through
CC       the floor plate. Expressed in cells of the retinal ganglion cell
CC       layer during retinal axon guidance to the optic disk.
CC   -!- DEVELOPMENTAL STAGE: Expressed in the floor plate throughout the
CC       period of commissural axon pathfinding.
CC   -!- SIMILARITY: Belongs to the ephrin family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF025288; AAC53537.1; -.
DR   EMBL; BC052001; AAH52001.1; -.
DR   EMBL; BC058617; AAH58617.1; -.
DR   MGD; MGI:109196; Efnb3.
DR   GO; GO:0007628; P:adult walking behavior; IMP.
DR   GO; GO:0007411; P:axon guidance; IMP.
DR   InterPro; IPR008972; Cupredoxin.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;
KW   Signal.
FT   SIGNAL        1     27       POTENTIAL.
FT   CHAIN        28    340       EPHRIN-B3.
FT   DOMAIN       28    227       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    228    248       POTENTIAL.
FT   DOMAIN      249    340       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      338    340       PDZ RECOGNITION MOTIF (POTENTIAL).
FT   DISULFID     62    104       BY SIMILARITY.
FT   DISULFID     92    156       BY SIMILARITY.
FT   CARBOHYD    210    210       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   340 AA;  35884 MW;  52F3D58FD209A6B8 CRC64;

  Query Match             72.3%;  Score 1771;  DB 1;  Length 340;
  Best Local Similarity   95.6%;  Pred. No. 3.9e-109;
  Matches  323;  Conservative    7;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
              || || |||||:|||||||| ||||||||||||||||||||||||||||||||||||||
Db          1 MGAPHFGPGGVQVGALLLLGFAGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

Qy         61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
              |||||||||||||:|||||||| ||||||||||||||||||||||||||||||||||||
Db         61 LCPRARPPGPHSSPSYEFYKLYLVEGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy        121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180

Qy        181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
                |||||||||||||||| |||:: :||||:|||||||||||||||||||||||:|||||
Db        181 VSEMPMERDRGAAHSAEPGRDTIPGDPSSNATSRGAEGPLPPPSMPAVAGAAGGMALLLL 240

Qy        241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300

Qy        301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
                | ||||||||||||||||||||||||||||||||||
Db        301 GTADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
```

```
RESULT 3
EFB2_MOUSE
ID   EFB2_MOUSE     STANDARD;      PRT;   336 AA.
AC   P52800;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Ephrin-B2 precursor (EPH-related receptor tyrosine kinase ligand 5)
DE   (LERK-5) (HTK ligand) (HTK-L) (ELF-2).
GN   EFNB2 OR EPLG5 OR LERK5 OR HTKL OR ELF2 OR EPL5.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96145238; PubMed=8559144;
RA   Cerretti D.P., Vanden Bos T., Nelson N., Kozlosky C.J., Reddy P.,
RA   Maraskovsky E., Park L.S., Lyman S.D., Copeland N.G.,
RA   Gilbert D.J., Jenkins N.A., Fletcher R.A.;
RT   "Isolation of LERK-5: a ligand of the eph-related receptor tyrosine
RT   kinases.";
RL   Mol. Immunol. 32:1197-1205(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CB57BL/6J X SJL/J;
RX   MEDLINE=95199254; PubMed=7534404;
RA   Bennett B.D., Zeigler F.C., Gu Q., Fendly B., Goddard A.D.,
RA   Gillett N., Matthews W.;
RT   "Molecular cloning of a ligand for the EPH-related receptor protein-
RT   tyrosine kinase Htk.";
RL   Proc. Natl. Acad. Sci. U.S.A. 92:1866-1870(1995).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ICR; TISSUE=Brain;
RX   MEDLINE=95379837; PubMed=7651410;
RA   Bergemann A.D., Cheng H.J., Brambilla R., Klein R., Flanagan J.G.;
RT   "ELF-2, a new member of the Eph ligand family, is segmentally
RT   expressed in mouse embryos in the region of the hindbrain and newly
RT   forming somites.";
RL   Mol. Cell. Biol. 15:4921-4929(1995).
```

RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP FUNCTION.
RX MEDLINE=20171264; PubMed=10704386;
RA Imondi R., Wideman C., Kaprielian Z.;
RT "Complementary expression of transmembrane ephrins and their receptors
RT in the mouse spinal cord: a possible role in constraining the
RT orientation of longitudinally projecting axons.";
RL Development 127:1397-1410(2000).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (1.92 ANGSTROMS) OF 30-170.
RX MEDLINE=21563306; PubMed=11703926;
RA Toth J., Cutforth T., Gelinas A.D., Bethoney K.A., Bard J.,
RA Harrison C.J.;
RT "Crystal structure of an ephrin ectodomain.";
RL Dev. Cell 1:83-92(2001).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 31-168 IN COMPLEX WITH
RP EPHB2.
RX MEDLINE=21638766; PubMed=11780069;
RA Himanen J.-P., Rajashankar K.R., Lackmann M., Cowan C.A.,
RA Henkemeyer M., Nikolov D.B.;
RT "Crystal structure of an Eph receptor-ephrin complex.";
RL Nature 414:933-938(2001).
CC -!- FUNCTION: Binds to the receptor tyrosine kinases EPHB2 and EPHB4.
CC May play a role in constraining the orientation of longitudinally
CC projecting axons.
CC -!- SUBUNIT: Binds to the receptor tyrosine kinase EPHB4.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed on lateral floor plate cells,
CC specifically on commissural axon segments that have passed through
CC the floor plate. Expressed in cells of the retinal ganglion cell
CC layer during retinal axon guidance to the optic disk.
CC -!- DEVELOPMENTAL STAGE: Expressed in the floor plate throughout the

```
CC       period of commissural axon pathfinding.
CC   -!- PTM: Inducible phosphorylation of tyrosine residues in the
CC       cytoplasmic domain (By similarity).
CC   -!- SIMILARITY: Belongs to the ephrin family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U16819; AAA99708.1; -.
DR   EMBL; L38847; AAC42052.1; -.
DR   EMBL; U30244; AAA82934.1; -.
DR   EMBL; BC057009; AAH57009.1; -.
DR   PIR; I49766; I49766.
DR   PDB; 1IKO; 15-MAY-02.
DR   PDB; 1KGY; 28-MAY-02.
DR   MGD; MGI:105097; Efnb2.
DR   InterPro; IPR008972; Cupredoxin.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;
KW   Signal; Phosphorylation; 3D-structure.
FT   SIGNAL        1     28       POTENTIAL.
FT   CHAIN        29    336       EPHRIN-B2.
FT   DOMAIN       29    232       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    233    253       POTENTIAL.
FT   DOMAIN      254    336       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      334    336       PDZ RECOGNITION MOTIF (POTENTIAL).
FT   DISULFID     65    104
FT   DISULFID     92    156
FT   CARBOHYD     39     39       N-LINKED (GLCNAC. . .).
FT   CARBOHYD    142    142       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT      3      4       MISSING (IN REF. 3).
FT   CONFLICT    177    177       A -> T (IN REF. 1).
SQ   SEQUENCE   336 AA;  37202 MW;  D08894996E399554 CRC64;

  Query Match             25.7%;  Score 628.5;  DB 1;  Length 336;
  Best Local Similarity   41.8%;  Pred. No. 2.3e-34;
  Matches  137;  Conservative   49;  Mismatches  129;  Indels   13;  Gaps    5;

Qy         14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
              | |::|    :   : |||:|||||:| :|    | ||||||||:||::||:      :
Db         17 GLLMVLCRTAISRSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 73

Qy         74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
                ||:||:|:|   |  ||        || | ||| |::||||||||:|||||| ||: :
Db         74 GQYEYYKVYMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK 133

Qy        134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
              |||||:||:|: |||:: :|||| || ||:|::|||  |  | |    |     :|
```

```
Db        134 DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSARNHGPTRRPELEAGTN 193

Qy        191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
              | : :  |  :  ||  |   ::  :   |    :   || | |  : :: :      :
Db        194 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIIFIVIIITLVVLLL 253

Qy        251 WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
                ||| :    :|    |     :   ||        :|| :: | ||    ||  ||||
Db        254 KYRRRHRKHSPQHTTTLSLSTLATPKRGGNN----NGSEPSDVIIPLR---TADSVFCPH 306

Qy        311 YEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
              ||||||||||||||||: ||||| ||||
Db        307 YEKVSGDYGHPVYIVQEMPPQSPANIYY 334
```

```
RESULT 4
EFB1_HUMAN
ID   EFB1_HUMAN     STANDARD;      PRT;   346 AA.
AC   P98172;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Ephrin-B1 precursor (EPH-related receptor tyrosine kinase ligand 2)
DE   (LERK-2) (ELK ligand) (ELK-L).
GN   EFNB1 OR EPLG2 OR LERK2 OR EFL-3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=94349923; PubMed=8070404;
RA   Beckmann M.P., Cerretti D.P., Baum P., Vanden Bos T., James L.,
RA   Farrah T., Kozlosky C., Hollingsworth T., Shilling H., Maraskovsky E.,
RA   Fletcher F.A., Lhotak V., Pawson T., Lyman S.D.;
RT   "Molecular characterization of a family of ligands for eph-related
RT   tyrosine kinase receptors.";
RL   EMBO J. 13:3757-3762(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Davis S., Gale N.W., Aldrich T.H., Maisonpierre P.C., Lhotak V.,
RA   Pawson T., Goldfarb M., Yancopoulos G.D.;
RL   Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Fletcher F.A., Huebner K., Shaffer L.G., Monaco A., Mueller U.,
RA   Kozlosky C., Druck T., Simoneaux D.K., Fairweather N., Chelly J.,
RA   Cerretti D.P., Belmont J.W., Beckmann M.P., Lyman S.D.;
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Howden P.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Eye, and Skin;
```

```
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Binds to the receptor tyrosine kinases EPHB1 and EPHA1.
CC       Binds to, and induce the collapse of, commissural axons/growth
CC       cones in vitro. May play a role in constraining the orientation of
CC       longitudinally projecting axons (By similarity).
CC   -!- SUBUNIT: Binds GRIP1 and GRIP2.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: Heart, placenta, lung, liver, skeletal muscle,
CC       kidney, pancreas.
CC   -!- INDUCTION: By TNF-alpha.
CC   -!- PTM: Inducible phosphorylation of tyrosine residues in the
CC       cytoplasmic domain (By similarity).
CC   -!- SIMILARITY: Belongs to the ephrin family.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U09304; AAA53093.1; -.
DR   EMBL; L37361; AAA52369.1; -.
DR   EMBL; U09303; AAB41127.1; -.
DR   EMBL; AL136092; -; NOT_ANNOTATED_CDS.
DR   EMBL; BC016649; AAH16649.1; -.
DR   EMBL; BC052979; AAH52979.1; -.
DR   PIR; S46993; S46993.
DR   Genew; HGNC:3226; EFNB1.
DR   MIM; 300035; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0005625; C:soluble fraction; TAS.
DR   GO; GO:0005108; F:transmembrane ephrin; TAS.
DR   GO; GO:0007155; P:cell adhesion; TAS.
DR   GO; GO:0007267; P:cell-cell signaling; TAS.
DR   InterPro; IPR008972; Cupredoxin.
```

```
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;
KW   Signal; Phosphorylation.
FT   SIGNAL        1     24       POTENTIAL.
FT   CHAIN        25    346       EPHRIN-B1.
FT   DOMAIN       25    237       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    238    258       POTENTIAL.
FT   DOMAIN      259    346       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      344    346       PDZ RECOGNITION MOTIF (POTENTIAL).
FT   DISULFID     64    101       BY SIMILARITY.
FT   DISULFID     89    153       BY SIMILARITY.
FT   CARBOHYD    139    139       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   346 AA;  38006 MW;  473DD2F1A5BF89DE CRC64;

  Query Match             25.4%;  Score 623;  DB 1;  Length 346;
  Best Local Similarity   39.2%;  Pred. No. 5.4e-34;
  Matches  143;  Conservative   48;  Mismatches  116;  Indels   58;  Gaps    9;

Qy          8 PGGVRVGALLLLGVLGLVSGL------SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
              ||   :|  |:  |:  :  |      :|||| |:| | :| :  | |:||:|||:||:: 
Db          4 PGQRWLGKWLVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63

Qy         62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
              ||||    |     ||:||||||   |   |     ||:|:||:||: ::|||||||:| 
Db         64 CPRAEAGRP-----YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118

Qy        122 PNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
              ||  | ||: |||||| :||:|: |||| :|||| || ||::::||| |      :
Db        119 PNYMGLEFKKHHDYYITSTSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTT 178

Qy        182 SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
              |    | |     : : ||     ||      :   |    |       ||:|| :
Db        179 SRPSKEADNTVKMATQAPGSRGSLGDSDGKHETVNQEEKSGP-------GASGGSSGDPD 231

Qy        237 ------LLLLGVAGAGGA-------------MCWRRRRAKPSESRHPGPGSFGRGGSLGL 277
                    : |    |||                :  |:|  | ::          |  :| |
Db        232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLKLRKRHRKHTQQ---------RAAALSL 282

Qy        278 ----GGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
                  || |    || :: | ||     :  :|||||||||||||||||: |||||
Db        283 STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP 339

Qy        334 PNIYY 338
               ||||
Db        340 ANIYY 344


RESULT 5
EFB2_HUMAN
ID   EFB2_HUMAN     STANDARD;      PRT;   333 AA.
AC   P52799;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
```

```
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Ephrin-B2 precursor (EPH-related receptor tyrosine kinase ligand 5)
DE   (LERK-5) (HTK ligand) (HTK-L).
GN   EFNB2 OR EPLG5 OR LERK5 OR HTKL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=96145238; PubMed=8559144;
RA   Cerretti D.P., Vanden Bos T., Nelson N., Kozlosky C.J., Reddy P.,
RA   Maraskovsky E., Park L.S., Lyman S.D., Copeland N.G., Gilbert D.J.,
RA   Jenkins N.A., Fletcher R.A.;
RT   "Isolation of LERK-5: a ligand of the eph-related receptor tyrosine
RT   kinases.";
RL   Mol. Immunol. 32:1197-1205(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=95199254; PubMed=7534404;
RA   Bennett B.D., Zeigler F.C., Gu Q., Fendly B., Goddard A.D.,
RA   Gillett N., Matthews W.;
RT   "Molecular cloning of a ligand for the EPH-related receptor protein-
RT   tyrosine kinase Htk.";
RL   Proc. Natl. Acad. Sci. U.S.A. 92:1866-1870(1995).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98192220; PubMed=9533549;
RA   Vogt T., Stolz W., Welsh J., Jung B., Kerbel R.S., Kobayashi H.,
RA   Landthaler M., McClelland M.;
RT   "Overexpression of Lerk-5/Eplg5 messenger RNA: a novel marker for
RT   increased tumorigenicity and metastatic potential in human malignant
RT   melanomas.";
RL   Clin. Cancer Res. 4:791-797(1998).
CC   -!- FUNCTION: Binds to the receptor tyrosine kinases EPHB4 and EPHA3.
CC       May play a role in constraining the orientation of longitudinally
CC       projecting axons (By similarity).
CC   -!- SUBUNIT: Binds to the receptor tyrosine kinases EPHB4 and EPHA3.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: Lung and kidney.
CC   -!- PTM: Inducible phosphorylation of tyrosine residues in the
CC       cytoplasmic domain (By similarity).
CC   -!- SIMILARITY: Belongs to the ephrin family.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U16797; AAA99707.1; -.
DR   EMBL; L38734; AAC41752.1; -.
DR   EMBL; U81262; AAD03786.1; -.
```

```
DR   PIR; I84743; I84743.
DR   Genew; HGNC:3227; EFNB2.
DR   MIM; 600527; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0005106; F:ephrin; TAS.
DR   GO; GO:0005108; F:transmembrane ephrin; TAS.
DR   GO; GO:0007267; P:cell-cell signaling; TAS.
DR   GO; GO:0007397; P:histogenesis and organogenesis; TAS.
DR   InterPro; IPR008972; Cupredoxin.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;
KW   Signal; Phosphorylation.
FT   SIGNAL        1     27       POTENTIAL.
FT   CHAIN        28    333       EPHRIN-B2.
FT   DOMAIN       28    229       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    230    250       POTENTIAL.
FT   DOMAIN      251    333       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      331    333       PDZ RECOGNITION MOTIF (POTENTIAL).
FT   DISULFID     62    101       BY SIMILARITY.
FT   DISULFID     89    153       BY SIMILARITY.
FT   CARBOHYD     36     36       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    139    139       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   333 AA;  36923 MW;  6D9932A632626AEA CRC64;

  Query Match             25.3%;  Score 620.5;  DB 1;  Length 333;
  Best Local Similarity   40.5%;  Pred. No. 7.6e-34;
  Matches  133;  Conservative   52;  Mismatches  130;  Indels   13;  Gaps    5;

Qy         14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
              | |::|    :   : |||:||||:| :|    | |||||||:||::||:       :
Db         14 GVLMVLCRTAISKSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 70

Qy         74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
                ||:||:|:|   |  ||        || | :|| |::|||||||:|||||| ||: :
Db         71 GQYEYYKVYMVDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK 130

Qy        134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
              |||||:||:|: |||:: :|||| || ||:|::|||  |  |    : |     :|
Db        131 DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN 190

Qy        191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
              | : :  |  :  ||  |   ::  :   :    :   || | |  : :: :      :
Db        191 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLL 250

Qy        251 WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
                |||  :    :|    |     :    |        :|| :: | ||    ||  ||||
Db        251 KYRRRHRKHSPQHTTTLSLSTLATPKRSGNN----NGSEPSDIIIPLR---TADSVFCPH 303

Qy        311 YEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
              |||||||||||||||: ||||| ||||
Db        304 YEKVSGDYGHPVYIVQEMPPQSPANIYY 331
```

RESULT 6
EFB1_CHICK
ID   EFB1_CHICK   STANDARD;   PRT;   334 AA.
AC   O73612;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Ephrin-B1 precursor (CEK5 ligand) (CEL5-L).
GN   EFNB1.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97223524; PubMed=9070326;
RA   Holash J.A., Soans C., Chong L.D., Shao H., Dixit V.M.,
RA   Pasquale E.B.;
RT   "Reciprocal expression of the Eph receptor Cek5 and its ligand(s) in
RT   the early retina.";
RL   Dev. Biol. 182:256-269(1997).
CC   -!- SUBUNIT: Binds to the receptor tyrosine kinase EPHB2.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- PTM: Inducible phosphorylation of tyrosine residues in the
CC   cytoplasmic domain (By similarity).
CC   -!- SIMILARITY: Belongs to the ephrin family.
CC   --
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --
DR   EMBL; U72394; AAC07986.1; -.
DR   InterPro; IPR008972; Cupredoxin.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;
KW   Signal; Phosphorylation.
FT   SIGNAL   1   25   POTENTIAL.
FT   CHAIN   26   334   EPHRIN-B1.
FT   DOMAIN   26   231   EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   232   252   POTENTIAL.
FT   DOMAIN   253   334   CYTOPLASMIC (POTENTIAL).
FT   DOMAIN   332   334   PDZ RECOGNITION MOTIF (POTENTIAL).
FT   DISULFID   60   97   BY SIMILARITY.
FT   DISULFID   85   149   BY SIMILARITY.
FT   CARBOHYD   135   135   N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   334 AA; 36858 MW; 48AF556E9ED56CD5 CRC64;

  Query Match   25.3%; Score 619; DB 1; Length 334;

```
  Best Local Similarity   39.3%;  Pred. No. 9.5e-34;
  Matches  144;  Conservative   50;  Mismatches  100;  Indels   72;  Gaps   13;

Qy          8 PGGVR--VGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRA 65
              | | |  :| || |  |      ||||| |:: | :| :  | |:||:|||:||::||:|
Db          4 PRGGRWLLGVLLALCRLAAPLAKSLEPVSWSAGNPKFMSGKGLVIYPEIGDKLDIICPKA 63

Qy         66 RPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLW 125
               |  |     |::||||||   |   |     ||:|:||:||: ::|||||||||:|||
Db         64 EPSKP-----YDYYKLYLVKKDQADACSTVMDPNVLVTCNRPEQEIRFTIKFQEFSPNYM 118

Qy        126 GHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMP 185
               | ||:   ||:| :||:|| :|||: :|||| || ||::::||| |    :| :  :  |
Db        119 GLEFKRQQDYFITSTSNGTLDGLENREGGVCQTRSMKIVMKVGQDP-NAVIPEQLTTSRP 177

Qy        186 MER--------DRGAAHSL----EPGKENLPGDPTSNA--TSRGAEGPLPPPSMPAVAGA 231
               :          :   | :    ||||   ||    |   |   ::| |   |  ||  |
Db        178 SKEADNTVKIVTQSPRHKVPTVEEPGK---PGSVNQNGQETQGPSDGFL--SSKVAVFAA 232

Qy        232 AGG-----------LALLLLGVAGAGGAMCWRRRRAKPSESRH--------PGPGSFGRG 272
               |           | :||: :         |:|  | :: |           |   |
Db        233 IGAGCVIFILIIIFLVVLLIKI---------RKRHRKHTQQRAAALSLSTLASPKCSGNA 283

Qy        273 GSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQS 332
               ||              || :: | ||     :  :||||||||||||||||||: ||||
Db        284 GS--------------EPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQS 326

Qy        333 PPNIYY 338
               | ||||
Db        327 PANIYY 332
```

```
RESULT 7
EFB2_BRARE
ID   EFB2_BRARE     STANDARD;      PRT;   332 AA.
AC   O73874;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Ephrin-B2 precursor (Ephrin B2a).
GN   EFNB2 OR EFNB2A.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98438455; PubMed=9765210;
RA   Durbin L., Brennan C., Shiomi K., Cooke J., Barrios A.,
RA   Shanmugalingam S., Guthrie B., Lindberg R., Holder N.;
RT   "Eph signaling is required for segmentation and differentiation of
RT   the somites.";
RL   Genes Dev. 12:3096-3109(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21290827; PubMed=11397014;
```

```
RA   Chan J., Mably J.D., Serluca F.C., Chen J.N., Goldstein N.B.,
RA   Thomas M.C., Cleary J.A., Brennan C., Fishman M.C., Roberts T.M.;
RT   "Morphogenesis of prechordal plate and notochord requires intact
RT   eph/ephrin b signaling.";
RL   Dev. Biol. 234:470-482(2001).
CC   -!- SUBUNIT: Binds to the receptor tyrosine kinase EPHB4.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- PTM: Inducible phosphorylation of tyrosine residues in the
CC       cytoplasmic domain (By similarity).
CC   -!- SIMILARITY: Belongs to the ephrin family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AJ004863; CAA06168.1; -.
DR   EMBL; AF375225; AAK64275.1; -.
DR   ZFIN; ZDB-GENE-990415-67; efnb2a.
DR   InterPro; IPR008972; Cupredoxin.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;
KW   Signal; Phosphorylation.
FT   SIGNAL        1     24       POTENTIAL.
FT   CHAIN        25    332       EPHRIN-B2.
FT   DOMAIN       25    225       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    226    246       POTENTIAL.
FT   DOMAIN      247    332       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      330    332       PDZ RECOGNITION MOTIF (POTENTIAL).
FT   DISULFID     59     98       BY SIMILARITY.
FT   DISULFID     86    150       BY SIMILARITY.
FT   CARBOHYD     20     20       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     33     33       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    136    136       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    211    211       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   332 AA;  36724 MW;  189ED82372C71C8B CRC64;
```

```
  Query Match             25.2%;  Score 617.5;  DB 1;  Length 332;
  Best Local Similarity   41.8%;  Pred. No. 1.2e-33;
  Matches  143;  Conservative   54;  Mismatches  106;  Indels   39;  Gaps   12;

Qy         14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
              | |::   : |   | |: :|||: | :|    | ||||||||::|::|||      |
Db         11 GVLVIACKVNLSRALILDSIYWNTTNTKFVPGQGLVLYPQIGDKMDIVCPRVE---GGSM 67

Qy         74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
                 |:|||||:|   | : |:   |   || | :|| |::||:||||:|||||| ||
Db         68 EGVEYYKLYMVPLEQLKSCQVTKADTPLLNCVKPDQDVKFTLKFQEFSPNLWGLEFFRGK 127

Qy        134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRK-PVSEMPMERDRGA 192
```

```
                |||||:||:|| |||:: :|||| |: ||::::|||:|     |:  | |  |   | |
Db        128 DYYIISTSNGTMEGLDNQEGGVCKTKSMKIIMKVGQNPSDPISPKDYPTSYPPKHPDLGG 187

Qy        193 AHS-----LEP-----GKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGV 242
                |     |:|     |::   ||   :::  |:|  |       :| |:  : :::: :
Db        188 KDSKSNEVLKPDASPHGEDK--GDGNKSSSVIGSEVAL----FACIASASVIVIIIIIML 241

Qy        243 AGAGGAMCWRRRRAKPSESRHPGPGSFG------RGGSLGLGGGGGMGPREAEPGELGIA 296
                  : :|||  | |  :|    |        ||||    ||   |   :|| :: |
Db        242 VFL--LLKYRRRHRKHS-PQHATTLSLSTLATPKRGGS----GGNNNG---SEPSDIIIP 291

Qy        297 LRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
                ||    ||  |||||||||||||||||||: ||||| ||||
Db        292 LR---TADSVFCPHYEKVSGDYGHPVYIVQEMPPQSPANIYY 330
```

```
RESULT 8
EFB1_MOUSE
ID   EFB1_MOUSE     STANDARD;      PRT;   345 AA.
AC   P52795;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Ephrin-B1 precursor (EPH-related receptor tyrosine kinase ligand 2)
DE   (LERK-2) (ELK ligand) (ELK-L) (STRA1 protein) (CEK5 receptor ligand)
DE   (CEK5-L).
GN   EFNB1 OR EPLG2 OR LERK2 OR STRA1 OR EPL2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/Sv;
RX   MEDLINE=95203867; PubMed=7896266;
RA   Fletcher F.A., Renshaw B., Hollingsworth T., Baum P., Lyman S.D.,
RA   Jenkins N.A., Gilbert D.J., Copeland N.G., Davison B.L.;
RT   "Genomic organization and chromosomal localization of mouse Eplg2, a
RT   gene encoding a binding protein for the receptor tyrosine kinase
RT   elk.";
RL   Genomics 24:127-132(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95377533; PubMed=7649373;
RA   Bouillet P., Oulad-Abdelghani M., Vicaire S., Garnier J.M.,
RA   Schuhbaur B., Dolle P., Chambon P.;
RT   "Efficient cloning of cDNAs of retinoic acid-responsive genes in P19
RT   embryonal carcinoma cells and characterization of a novel mouse gene,
RT   Stra1 (mouse LERK-2/Eplg2).";
RL   Dev. Biol. 170:420-433(1995).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=95014510; PubMed=7929389;
RA   Shao H., Lou L., Pandey A., Pasquale E.B., Dixit V.M.;
RT   "cDNA cloning and characterization of a ligand for the Cek5 receptor
RT   protein-tyrosine kinase.";
```

RL J. Biol. Chem. 269:26606-26609(1994).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP FUNCTION.
RX MEDLINE=20171264; PubMed=10704386;
RA Imondi R., Wideman C., Kaprielian Z.;
RT "Complementary expression of transmembrane ephrins and their receptors
RT in the mouse spinal cord: a possible role in constraining the
RT orientation of longitudinally projecting axons.";
RL Development 127:1397-1410(2000).
CC -!- FUNCTION: Binds to the receptor tyrosine kinases EPHB1 and EPHA1.
CC Binds to, and induce the collapse of, commissural axons/growth
CC cones in vitro. May play a role in constraining the orientation of
CC longitudinally projecting axons.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed on lateral floor plate cells,
CC specifically on commissural axon segments that have passed through
CC the floor plate. Expressed in cells of the retinal ganglion cell
CC layer during retinal axon guidance to the optic disc.
CC -!- DEVELOPMENTAL STAGE: Expressed in the floor plate throughout the
CC period of commissural axon pathfinding.
CC -!- PTM: Inducible phosphorylation of tyrosine residues in the
CC cytoplasmic domain.
CC -!- SIMILARITY: Belongs to the ephrin family.
CC --
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC --
DR EMBL; U07602; AAC53247.1; -.

```
DR   EMBL; U07598; AAC53247.1; JOINED.
DR   EMBL; U07599; AAC53247.1; JOINED.
DR   EMBL; U07600; AAC53247.1; JOINED.
DR   EMBL; Z48781; CAA88695.1; -.
DR   EMBL; U12983; AAA53231.1; -.
DR   EMBL; BC006797; AAH06797.1; -.
DR   PIR; I48780; I48780.
DR   MGD; MGI:102708; Efnb1.
DR   GO; GO:0045121; C:lipid raft; IDA.
DR   GO; GO:0007411; P:axon guidance; IMP.
DR   InterPro; IPR008972; Cupredoxin.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;
KW   Signal; Phosphorylation.
FT   SIGNAL        1     24       POTENTIAL.
FT   CHAIN        25    345       EPHRIN-B1.
FT   DOMAIN       25    236       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    237    257       POTENTIAL.
FT   DOMAIN      258    345       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      343    345       PDZ RECOGNITION MOTIF (POTENTIAL).
FT   DISULFID     64    101       BY SIMILARITY.
FT   DISULFID     89    153       BY SIMILARITY.
FT   CARBOHYD    139    139       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT     90     90       S -> T (IN REF. 2).
SQ   SEQUENCE   345 AA;  37859 MW;  8C96FD3DC5CBC405 CRC64;

  Query Match             24.7%;  Score 604.5;  DB 1;  Length 345;
  Best Local Similarity   37.9%;  Pred. No. 8.7e-33;
  Matches  136;  Conservative   51;  Mismatches  107;  Indels   65;  Gaps   10;

Qy         15 ALLLLGVLGLVSGL--SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHS 72
              |:::| :  | : |  :|||| |:| | :| :  | |:||:|||:||::|||| |
Db         15 AMVVLTLCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDIICPRAEAGRP-- 72

Qy         73 SPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSH 132
                 ||:|||||| |  |    ||:|:||::| ::|||||||||:||| | ||: :
Db         73 ---YEYYKLYLVRPEQAAACSTVLDPNVLVTCNKPHQEIRFTIKFQEFSPNYMGLEFKKY 129

Qy        133 HDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGA 192
              ||||| :||:|: |||||: :|||| || ||::::||| |     | :  :  | :
Db        130 HDYYITSTSNGSLEGLENREGGVCRTRTMKIVMKVGQDP-NAVTPEQLTTSRPSKESDNT 188

Qy        193 AHSLEPGKENLPGDPTSNATSRGAEGP---------LPPPSMPAVAGAAGG-------LA 236
               :           : |  ||::|             | |   |   |
Db        189 VKT------------ATQAPGRGSQGDSDGKHETVNQEEKSGPGAGGGGSGDSDSFFNSK 236

Qy        237 LLLLGVAGAGGA-------------MCWRRRRAKPSESRHPGPGSFGRGGSLGL----GG 279
              : |    |||               :  |:|  | ::          |  :| |
Db        237 VALFAAVGAGCVIFLLIIIFLTVLLLKLRKRHRKHTQQ---------RAAALSLSTLASP 287

Qy        280 GGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
               || |    || :: | ||     :  :|||||||||||||||||: ||||| ||||
Db        288 KGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSPANIYY 343
```

```
RESULT 9
EFB1_RAT
ID   EFB1_RAT       STANDARD;      PRT;   345 AA.
AC   P52796;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Ephrin-B1 precursor (EPH-related receptor tyrosine kinase ligand 2)
DE   (LERK-2) (ELK ligand) (ELK-L).
GN   EFNB1 OR EPLG2 OR LERK2.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=95022634; PubMed=7936648;
RA   Fletcher F.A., Carpenter M., Shilling H., Baum P., Ziegler S.,
RA   Gimpel S., Hollingsworth T., Vanden Bos T., Davison B.L.,
RA   Lyman S.D., Beckmann M.P.;
RT   "LERK-2, a binding protein for the receptor-tyrosine kinase ELK, is
RT   evolutionarily conserved and expressed in a developmentally regulated
RT   pattern.";
RL   Oncogene 9:3241-3248(1994).
CC   -!- FUNCTION: Binds to the receptor tyrosine kinases EPHB3
CC       (preferred), EPHB1 and EPHA1. Binds to, and induce the collapse
CC       of, commissural axons/growth cones in vitro. May play a role in
CC       constraining the orientation of longitudinally projecting axons
CC       (By similarity).
CC   -!- SUBUNIT: Binds to the receptor tyrosine kinases EPHB3 (preferred),
CC       EPHB1 and EPHB2.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- PTM: Inducible phosphorylation of tyrosine residues in the
CC       cytoplasmic domain (By similarity).
CC   -!- SIMILARITY: Belongs to the ephrin family.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U07560; AAA53092.1; -.
DR   PIR; I58406; I58406.
DR   InterPro; IPR008972; Cupredoxin.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;
KW   Signal; Phosphorylation.
```

```
FT   SIGNAL        1     24       POTENTIAL.
FT   CHAIN        25    345       EPHRIN-B1.
FT   DOMAIN       25    236       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    237    257       POTENTIAL.
FT   DOMAIN      258    345       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      343    345       PDZ RECOGNITION MOTIF (POTENTIAL).
FT   DISULFID     64    101       BY SIMILARITY.
FT   DISULFID     89    153       BY SIMILARITY.
FT   CARBOHYD    139    139       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   345 AA;  37951 MW;  1B3045C5C7358F7E CRC64;

  Query Match             24.5%;  Score 599.5;  DB 1;  Length 345;
  Best Local Similarity   37.6%;  Pred. No. 1.9e-32;
  Matches  135;  Conservative   52;  Mismatches  107;  Indels   65;  Gaps   10;

Qy         15 ALLLLGVLGLVSGL--SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHS 72
              |:::| :  | : |  :|||| |:| | :| :  | |:||:|||:||::|||| |
Db         15 AMVVLTLCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDIICPRAEAGRP-- 72

Qy         73 SPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSH 132
                ||:||||||  |   |    ||:|:||::| ::|||||||||:|||  | ||: :
Db         73 ---YEYYKLYLVRPEQAAACSTVLDPNVLVTCNKPQQEIRFTIKFQEFSPNYMGLEFKKY 129

Qy        133 HDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGA 192
              ||||| :||:|: |||||: :|||| || ||::::||| |     | :  :  | :
Db        130 HDYYITSTSNGSLEGLENREGGVCRTRTMKIVMKVGQDP-NAVTPEQLTTSRPSKESDNT 188

Qy        193 AHSLEPGKENLPGDPTSNATSRGAEGP---------LPPPSMPAVAGAAGG-------LA 236
               :            : |  ||::|             | |   |:  |
Db        189 VKT------------ATQAPGRGSQGDSDGKHETVNQQEKSGPGAGGSGSGDTDSFFNSK 236

Qy        237 LLLLGVAGAGGA-------------MCWRRRRAKPSESRHPGPGSFGRGGSLGL----GG 279
              : |    |||               :  |:|  | ::          |  :| |
Db        237 VALFAAVGAGCVIFLLIIIFLTVLLLKLRKRHRKHTQQ---------RAAALSLSTLASP 287

Qy        280 GGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
               |  |    || :: | ||     :  :||||||||||||||||||: ||||| ||||
Db        288 KGDSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSPANIYY 343


RESULT 10
EFB1_XENLA
ID   EFB1_XENLA     STANDARD;      PRT;   327 AA.
AC   O13097;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Ephrin-B1 precursor (EPH-related receptor tyrosine kinase ligand 2)
DE   (LERK-2) (ELK ligand) (ELK-L) (XLERK).
GN   EFNB1 OR EPLG2 OR LERK2.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
```

```
RX   MEDLINE=97316777; PubMed=9174051;
RA   Jones T.L., Karavanova I., Chong L., Zhou R.P., Daar I.O.;
RT   "Identification of XLerk, an Eph family ligand regulated during
RT   mesoderm induction and neurogenesis in Xenopus laevis.";
RL   Oncogene 14:2159-2166(1997).
CC   -!- FUNCTION: May have a role in the developing mesenchymal and
CC       nervous tissue.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: In the adult, expressed at low levels in most
CC       adult tissues with increased levels observed in the kidney,
CC       oocytes, ovary and testis.
CC   -!- PTM: Inducible phosphorylation of tyrosine residues in the
CC       cytoplasmic domain (By similarity).
CC   -!- SIMILARITY: Belongs to the ephrin family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U31427; AAC35995.1; -.
DR   InterPro; IPR008972; Cupredoxin.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;
KW   Signal; Phosphorylation.
FT   SIGNAL        1     20       POTENTIAL.
FT   CHAIN        21    327       EPHRIN-B1.
FT   DOMAIN       21    225       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    226    246       POTENTIAL.
FT   DOMAIN      247    327       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      325    327       PDZ RECOGNITION MOTIF (POTENTIAL).
FT   DISULFID     57     93       BY SIMILARITY.
FT   DISULFID     81    145       BY SIMILARITY.
FT   CARBOHYD    131    131       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    202    202       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   327 AA;  36621 MW;  71230CE7F6BE5974 CRC64;

  Query Match             24.1%;  Score 591;  DB 1;  Length 327;
  Best Local Similarity   39.5%;  Pred. No. 6.3e-32;
  Matches  144;  Conservative   43;  Mismatches  100;  Indels   78;  Gaps   12;

Qy         10 GVR--VGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRA-- 65
              |:|  :| ||:|  |    | :|||| ||| | || :  | ||||:||||||::||:
Db          3 GLRRLLGLLLVLYRLCSALGKNLEPVTWNSQNPRFISGKGLVLYPEIGDRLDIICPKGLF 62

Qy         66 RPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLW 125
              :|        ||:|||||:|   |   |     ||:|:||::|  : |||||||:|||
Db         63 QP--------YEYYKLYMVRRDQLEACSTVIDPNVLVTCNQPGKEYRFTIKFQEFSPNYM 114

Qy        126 GHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMP 185
```

```
                | ||| : |||| :||: | :|||: :|||| || ||:::::||| |   ||| : ::
Db        115 GLEFRRNQDYYITSTSNSTLQGLENREGGVCQTRSMKIIMKVGQDP--NAVPPEQLT--- 169

Qy        186 MERDRGAAHSLEPGKENLPGDPTSNATSRGA-EGPLPPP--------SMPAVAGAAGGLA 236
                      :  | ||    | |    : |   ||:  |          |       |
Db        170 ---------TTRPSKE---ADNTGKIATFGPWNGPVQNPGKSDTNLSDKPTGRWGVDGFF 217

Qy        237 LLLLGVAGAGGAMC----------------WRRRRAKPSE-------SRHPGPGSFGRGG 273
                 : |  | || |                  |:|  | ::       |    |   | |
Db        218 NSKIAVFAAIGAGCVIFILIIIFLVVLLIKIRKRHRKHTQQAAALSLSTLASPKCSGNAG 277

Qy        274 SLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
                |              || :: | ||     :  :||||||||||||||||||: |||||
Db        278 S--------------EPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP 320

Qy        334 PNIYY 338
                ||||
Db        321 ANIYY 325
```

```
RESULT 11
EFA2_BRARE
ID   EFA2_BRARE     STANDARD;      PRT;   195 AA.
AC   P79727;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Ephrin-A2 precursor (EPH-related receptor tyrosine kinase ligand 6)
DE   (LERK-6) (ELF-1) (ZFEPHL3).
GN   EFNA2 OR EPLG6 OR LERK6.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=97195707; PubMed=9043080;
RA   Brennan C., Monschau B., Lindberg R., Guthrie B., Drescher U.,
RA   Bonhoeffer F., Holder N.;
RT   "Two Eph receptor tyrosine kinase ligands control axon growth and may
RT   be involved in the creation of the retinotectal map in the
RT   zebrafish.";
RL   Development 124:655-664(1997).
CC   -!- FUNCTION: Control axon growth and may be involved in the creation
CC       of the retino-tectal map.
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC       (Potential).
CC   -!- TISSUE SPECIFICITY: Widespread expression in the embryo.
CC   -!- DEVELOPMENTAL STAGE: Expressed in the presumptive midbrain of
CC       developing embryos from the six-somite stage. By 24 hours,
CC       expressed throughout the midbrain including the region of the
CC       presumptive tectum. At later stages, expressed in a graded fashion
CC       throughout the tectum.
CC   -!- SIMILARITY: Belongs to the ephrin family.
CC   ---------------------------------------------------------------------
```

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC ----------
DR EMBL; Y09668; CAA70863.1; -.
DR ZFIN; ZDB-GENE-990415-66; efna2.
DR InterPro; IPR008972; Cupredoxin.
DR InterPro; IPR001799; Ephrin.
DR Pfam; PF00812; Ephrin; 1.
DR PRINTS; PR01347; EPHRIN.
DR ProDom; PD002533; Ephrin; 1.
DR PROSITE; PS01299; EPHRIN; 1.
KW Developmental protein; Neurogenesis; Glycoprotein; Lipoprotein;
KW Membrane; GPI-anchor; Signal.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 174 EPHRIN-A2.
FT PROPEP 175 195 REMOVED IN MATURE FORM (POTENTIAL).
FT DISULFID 57 97 BY SIMILARITY.
FT LIPID 174 174 GPI-anchor amidated cysteine (Potential).
FT CARBOHYD 32 32 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 195 AA; 22688 MW; 9EE284FEB61D0C42 CRC64;

Query Match 7.6%; Score 185; DB 1; Length 195;
Best Local Similarity 29.9%; Pred. No. 1.4e-05;
Matches 63; Conservative 21; Mismatches 71; Indels 56; Gaps 7;

```
Qy          33 VYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRC 92
               |||||:| ||  :| | :   | | ||: ||    | |||    | | |::|       |
Db          29 VYWNSSNSRFW-QGEYTVAVSINDYLDVYCPYYESPQPHS--RMERYILFMVNHDGYLTC 85

Qy          93 EAPPAPNLLLTCDR---PDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGTREGLE 149
               |          |:|   ||  |||: ||| ::|   | |||  |:|| |::      |
Db          86 EHRMRGFKRWECNRPQSPDGPLRFSEKFQLFTPFSLGFEFRPGHEYYYISSPHPNHAGKP 145

Qy         150 SLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTS 209
                |:        :|| :             || |                | |:     |
Db         146 CLK--------LKVYV-------------KPTSS---------------GYESPEPFLTD 169

Qy         210 NATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
                :   ||:||               ||:|:|
Db         170 QSQRCGADGPC--------------LAVLML 186
```

RESULT 12
EFA3_HUMAN
ID EFA3_HUMAN STANDARD; PRT; 238 AA.
AC P52797;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Ephrin-A3 precursor (EPH-related receptor tyrosine kinase ligand 3)
DE (LERK-3) (EHK1 ligand) (EHK1-L).
GN EFNA3 OR EPLG3 OR LERK3 OR EFL2.

```
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95140419; PubMed=7838529;
RA   Kozlosky C.J., Maraskovsky E., McGrew J.T., Vanden Bos T.,
RA   Teepe M., Lyman S.D., Srinivasan S., Fletcher F.A., Gayle R.B. III,
RA   Cerretti D.P., Beckmann M.P.;
RT   "Ligands for the receptor tyrosine kinases hek and elk: isolation of
RT   cDNAs encoding a family of proteins.";
RL   Oncogene 10:299-306(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95063919; PubMed=7973638;
RA   Davis S., Gale N.W., Aldrich T.H., Maisonpierre P.C., Lhotak V.,
RA   Pawson T., Goldfarb M., Yancopoulos G.D.;
RT   "Ligands for EPH-related receptor tyrosine kinases that require
RT   membrane attachment or clustering for activity.";
RL   Science 266:816-819(1994).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Duodenum;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC   -!- TISSUE SPECIFICITY: Expressed in brain, skeletal muscle, spleen,
CC       thymus, prostate, testis, ovary, small intestine, and peripheral
CC       blood leukocytes.
CC   -!- SIMILARITY: Belongs to the ephrin family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
```

```
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U14187; AAC50078.1; -.
DR   EMBL; L37360; AAA52368.1; -.
DR   EMBL; BC017722; AAH17722.1; -.
DR   PIR; I38849; I38849.
DR   Genew; HGNC:3223; EFNA3.
DR   MIM; 601381; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0005005; F:transmembrane-ephrin receptor activity; TAS.
DR   GO; GO:0007267; P:cell-cell signaling; TAS.
DR   InterPro; IPR008972; Cupredoxin.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Glycoprotein; Lipoprotein; Membrane; GPI-anchor; Signal.
FT   SIGNAL        1     22       POTENTIAL.
FT   CHAIN        23    214       EPHRIN-A3.
FT   PROPEP      215    238       REMOVED IN MATURE FORM (POTENTIAL).
FT   DISULFID     63    110       BY SIMILARITY.
FT   LIPID       214    214       GPI-anchor amidated glycine (Potential).
FT   CARBOHYD     38     38       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     67     67       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    100    100       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT     71     74       MISSING (IN REF. 2).
SQ   SEQUENCE   238 AA;  26350 MW;  8EFD6AE8FE33FDDA CRC64;

  Query Match             7.3%;  Score 179;  DB 1;  Length 238;
  Best Local Similarity   28.4%;  Pred. No. 4.2e-05;
  Matches   65;  Conservative   24;  Mismatches   80;  Indels   60;  Gaps   12;

Qy          7 GPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCP--R 64
              |||           | ||     :   |||||:|:  : | || :   : | ||: ||
Db         24 GPG----------GALG-----NRHAVYWNSSNQHLRRE-GYTVQVNVNDYLDIYCPHYN 67

Qy         65 ARPPGPHSSP----NYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKF 117
              :   || : |      | | ||:|     | | |          |:||      ::|: ||
Db         68 SSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFK-RWECNRPHAPHSPIKFSEKF 126

Qy        118 QEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVP 177
              | ||    |:|| : |:|| |:|               ||   ||| :    :   |
Db        127 QRYSAFSLGYEFHAGHEYYYISTPTHNLH-------WKCLR--MKVFVCCASTSHSG--- 174

Qy        178 RKPVSEMP---------------MERDRGAAHSLE-------PGKENLP 204
               |||  :|                | :      ||       | :|:||
Db        175 EKPVPTLPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLP 223


RESULT 13
EFA2_MOUSE
ID   EFA2_MOUSE     STANDARD;      PRT;   209 AA.
AC   P52801;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
```

```
DE   Ephrin-A2 precursor (EPH-related receptor tyrosine kinase ligand 6)
DE   (LERK-6) (ELF-1) (CEK7-ligand) (CEK7-L).
GN   EFNA2 OR EPLG6 OR LERK6 OR ELF1 OR EPL6.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Swiss Webster; TISSUE=Brain;
RX   MEDLINE=95007776; PubMed=7522971;
RA   Cheng H.J., Flanagan J.G.;
RT   "Identification and cloning of ELF-1, a developmentally expressed
RT   ligand for the Mek4 and Sek receptor tyrosine kinases.";
RL   Cell 79:157-168(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=95181289; PubMed=7876076;
RA   Shao H., Lou L., Pandey A., Verderame M.F., Siever D.A., Dixit V.M.;
RT   "cDNA cloning and characterization of a Cek7 receptor
RT   protein-tyrosine kinase ligand that is identical to the ligand
RT   (ELF-1) for the Mek-4 and Sek receptor protein-tyrosine kinases.";
RL   J. Biol. Chem. 270:3467-3470(1995).
CC   -!- SUBUNIT: Binds to the receptor tyrosine kinases EPHA3, EPHA4 and
CC       EPHA5.
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC       (Potential).
CC   -!- SIMILARITY: Belongs to the ephrin family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U14941; AAA53636.1; -.
DR   EMBL; U14752; AAA68520.1; -.
DR   PIR; A54984; A54984.
DR   MGD; MGI:102707; Efna2.
DR   InterPro; IPR008972; Cupredoxin.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Glycoprotein; Lipoprotein; Membrane; GPI-anchor; Signal.
FT   SIGNAL        1     20       POTENTIAL.
FT   CHAIN        21    184       EPHRIN-A2.
FT   PROPEP      185    209       REMOVED IN MATURE FORM (POTENTIAL).
FT   DISULFID     69    110       BY SIMILARITY.
FT   LIPID       184    184       GPI-anchor amidated asparagine
FT                                (Potential).
FT   CARBOHYD     38     38       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    170    170       N-LINKED (GLCNAC. . .) (POTENTIAL).
```

```
FT   CARBOHYD    184    184       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   209 AA;  23586 MW;  F1997545F25B9ABC CRC64;

  Query Match             7.2%;  Score 176;  DB 1;  Length 209;
  Best Local Similarity   29.3%;  Pred. No. 5.7e-05;
  Matches   58;  Conservative   19;  Mismatches   69;  Indels   52;  Gaps    7;

Qy         33 VYWNSANKRFQAE-----GGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGA 87
              |||| :| |||       ||| :   | | ||: ||    | |  :   | | ||:| |
Db         35 VYWNRSNPRFQVSAVGDGGGYTVEVSINDYLDIYCPHYGAPLP-PAERMERYILYMVNGE 93

Qy         88 QGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGT 144
                 |:          |:||      |:|: ||| ::|   | |||  |:|| |: :
Db         94 GHASCDHRQRGFKRWECNRPAAPGGPLKFSEKFQLFTPFSLGFEFRPGHEYYYISATP-- 151

Qy        145 REGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLP 204
                  :|    ||   :|| :|                                  |  | |
Db        152 ----PNLVDRPCLR--LKVYVR-----------------------------PTNETLY 174

Qy        205 GDP----TSNATSRGAEG 218
              |    |||::  |  |
Db        175 EAPEPIFTSNSSCSGLGG 192


RESULT 14
EFA2_HUMAN
ID   EFA2_HUMAN     STANDARD;      PRT;   213 AA.
AC   O43921; O76020;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Ephrin-A2 precursor (EPH-related receptor tyrosine kinase ligand 6)
DE   (LERK-6) (HEK7-ligand) (HEK7-L).
GN   EFNA2 OR EPLG6 OR LERK6.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98126446; PubMed=9465306;
RA   Cerretti D.P., Nelson N.;
RT   "Characterization of the genes for mouse LERK-3/Ephrin-A3 (Epl3),
RT   mouse LERK-4/Ephrin-A4 (Epl4), and human LERK-6/Ephrin-A2 (EPLG6):
RT   conservation of intron/exon structure.";
RL   Genomics 47:131-135(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,
RA   Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen S.,
RA   Phan H., Velasco N., Garnes J., Danganan L., Poundstone P.,
RA   Christensen M., Georgescu A., Avila J., Liu S., Attix C., Andreise T.,
RA   Trankheim M., Amico-Keller G., Coefield J., Duarte S., Lucas S.,
RA   Bruce R., Thomas P., Quan G., Kronmiller B., Arellano A.,
RA   Montgomery M., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.O.,
RA   Carrano A.V.;
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
```

```
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=99045414; PubMed=9826538;
RA   Aasheim H.C., Pedeutour F., Grosgeorge J., Logtenberg T.;
RT   "Cloning, chromosal mapping, and tissue expression of the gene
RT   encoding the human Eph-family kinase ligand ephrin-A2.";
RL   Biochem. Biophys. Res. Commun. 252:378-382(1998).
CC   -!- SUBUNIT: Binds to the receptor tyrosine kinases EPHA3, EPHA4 and
CC       EPHA5.
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC       (Potential).
CC   -!- SIMILARITY: Belongs to the ephrin family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U92896; AAC39577.1; -.
DR   EMBL; U92893; AAC39577.1; JOINED.
DR   EMBL; U92894; AAC39577.1; JOINED.
DR   EMBL; AC004258; AAC04896.1; -.
DR   EMBL; AJ007292; CAA07435.1; -.
DR   PIR; JE0322; JE0322.
DR   Genew; HGNC:3222; EFNA2.
DR   MIM; 602756; -.
DR   GO; GO:0005106; F:ephrin; TAS.
DR   GO; GO:0007267; P:cell-cell signaling; TAS.
DR   InterPro; IPR008972; Cupredoxin.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Glycoprotein; Lipoprotein; Membrane; GPI-anchor; Signal.
FT   SIGNAL        1     24       POTENTIAL.
FT   CHAIN        25    188       EPHRIN-A2.
FT   PROPEP      189    213       REMOVED IN MATURE FORM (POTENTIAL).
FT   DISULFID     73    114       BY SIMILARITY.
FT   LIPID       188    188       GPI-anchor amidated asparagine
FT                                (Potential).
FT   CARBOHYD     42     42       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    174    174       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    188    188       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT      6      6       R -> A (IN REF. 3).
FT   CONFLICT     25     26       RA -> PP (IN REF. 3).
FT   CONFLICT     29     30       AA -> RR (IN REF. 3).
SQ   SEQUENCE   213 AA;  23878 MW;  33C9FB1A8168B2D0 CRC64;

  Query Match             7.2%;  Score 175.5;  DB 1;  Length 213;
  Best Local Similarity   36.8%;  Pred. No. 6.3e-05;
  Matches   43;  Conservative   14;  Mismatches   51;  Indels    9;  Gaps    3;
```

```
Qy          33 VYWNSANKRFQA-----EGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGA 87
               |||| :| || |      ||| :   | | ||: ||    | |  :   | | ||:| |
Db          39 VYWNRSNPRFHAGAGDDGGGYTVEVSINDYLDIYCPHYGAPLP-PAERMEHYVLYMVNGE 97

Qy          88 QGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHHDYYIIATS 141
                   |:          |:||      |:|: ||| ::|   | |||  |:|| |: :
Db          98 GHASCDHRQRGFKRWECNRPAAPGGPLKFSEKFQLFTPFSLGFEFRPGHEYYYISAT 154
```

```
RESULT 15
EFA2_CHICK
ID   EFA2_CHICK     STANDARD;      PRT;   200 AA.
AC   P52802;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Ephrin-A2 precursor (EPH-related receptor tyrosine kinase ligand 6)
DE   (LERK-6) (ELF-1).
GN   EFNA2 OR EPLG6 OR LERK6 OR ELF1.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95360981; PubMed=7634327;
RA   Cheng H.J., Nakamoto M., Bergemann A.D., Flanagan J.G.;
RT   "Complementary gradients in expression and binding of ELF-1 and Mek4
RT   in development of the topographic retinotectal projection map.";
RL   Cell 82:371-381(1995).
CC   -!- SUBUNIT: Binds to the receptor tyrosine kinases EPHA3, EPHA4 and
CC       EPHA5 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC       (Potential).
CC   -!- TISSUE SPECIFICITY: Expressed in a gradient across the tectum
CC       being more strongly expressed at the posterior pole.
CC   -!- SIMILARITY: Belongs to the ephrin family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L40932; AAC42229.1; -.
DR   InterPro; IPR008972; Cupredoxin.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Glycoprotein; Lipoprotein; Membrane; GPI-anchor; Signal.
FT   SIGNAL        1     22       POTENTIAL.
FT   CHAIN        23    175       EPHRIN-A2.
```

```
FT   PROPEP      176    200       REMOVED IN MATURE FORM (POTENTIAL).
FT   DISULFID     61    101       BY SIMILARITY.
FT   LIPID       175    175       GPI-anchor amidated asparagine
FT                                (Potential).
FT   CARBOHYD     36     36       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    161    161       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    175    175       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   200 AA;  23049 MW;  8FAB1AE5E45EED96 CRC64;

  Query Match             7.0%;  Score 172;  DB 1;  Length 200;
  Best Local Similarity   35.3%;  Pred. No. 0.0001;
  Matches   49;  Conservative   16;  Mismatches   58;  Indels   16;  Gaps    5;

Qy         15 ALLLLGVLGLVSGLSLEP---------VYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRA 65
              | ||  ::| |   | :|         |||| :| ||   | | :   | | ||: ||
Db          7 AALLAAIVG-VCVWSDDPGKVISDRYAVYWNRSNPRFH-RGDYTVEVSINDYLDIYCPHY 64

Qy         66 RPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSP 122
                | |  :   | | ||:|       |:          |:|||     |:|: ||| ::|
Db         65 EEPLP--AERMERYVLYMVNYEGHASCDHRQKGFKRWECNRPDSPSGPLKFSEKFQLFTP 122

Qy        123 NLWGHEFRSHHDYYIIATS 141
                | |||  |:|| |: |
Db        123 FSLGFEFRPGHEYYYISAS 141


Search completed: April 13, 2004, 09:25:55
Job time : 25.0377 secs
```